

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 16:46:47 ; Search time 83 Seconds
(without alignments)
260.082 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MARKSGDIEKIKKLVLL.....LAKPLTKDKIILINQLMDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158736573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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- 24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	678	100.0	136	20	AA1980
2	678	100.0	136	20	AA1981
3	538	79.4	142	21	AA1982
4	538	79.4	142	21	AA1983
5	515	76.0	142	20	AA1984
6	472	69.6	116	20	AA1985
7	437	64.5	104	21	AA1986
8	437	64.5	104	21	AA1987
9	301	44.4	70	21	AA1988

10	280	41.3	66	21	AA1989
11	213	31.4	71	21	AA1990
12	202	29.8	261	21	AA1991
13	192.5	28.4	67	20	AA1992
14	171.5	25.3	118	23	AA1993
15	156.5	23.1	471	24	AA1994
16	156.5	23.1	496	24	AA1995
17	156.5	23.1	666	24	AA1996
18	156.5	23.1	709	24	AA1997
19	156.5	23.1	719	24	AA1998
20	156.5	23.1	802	24	AA1999
21	156.5	23.1	870	24	AA2000
22	156.5	23.1	874	24	AA2001
23	156.5	23.1	887	24	AA2002
24	156.5	23.1	900	24	AA2003
25	156.5	23.1	906	24	AA2004
26	156.5	23.1	931	24	AA2005
27	155	22.9	922	22	AA2006
28	149	22.0	1373	23	AA2007
29	148.5	21.9	922	22	AA2008
30	148.5	21.9	922	22	AA2009
31	148.5	21.9	950	23	AA2010
32	146	21.5	1018	21	AA2011
33	141	20.8	1146	20	AA2012
34	139.5	20.6	1281	19	AA2013
35	139.5	20.6	1298	20	AA2014
36	139.5	20.6	1298	20	AA2015
37	139.5	20.6	1298	20	AA2016
38	137	20.2	125	23	AA2017
39	134.5	19.8	1122	23	AA2018
40	134	19.8	120	22	AA2019
41	133.5	19.7	1023	22	AA2020
42	131	19.3	136	23	AA2021
43	131	19.3	674	21	AA2022
44	130	19.2	1081	20	AA2023
45	130	19.2	1081	20	AA2024

ALIGNMENTS

RESULT 1

AA1980
ID AA1980 standard; Protein; 136 AA.

AC AA1980;

DT 10-JAN-2000 (first entry)

DE Brassica response regulator protein D22.

KW Signal transduction protein; dehiscence; male sterile plant; D22 gene; shatter resistance; oilseed rape; response regulator protein.

XX Brassica napus.

XX WO9949046-A1.

PD 30-SEP-1999.

XX 22-MAR-1999; 99WO-GB00905.

XX 20-MAR-1998; 98GB-0006113.

XX (BIOG-) BIOGENMA UK LTD.

XX Wyatt P, Roberts JA, Whitelaw C;

DR WPI; 1999-580449/49.

XX N-PSDB; AA222974.

PT A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants

PT
XX
PS
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

Claim 4; Fig 1; 71pp; English.

The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (*Brassica napus*). The present sequence represents a B. napus response regulator protein D22.

Query Match 100.0%; Score 678; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e-67;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 SFDLIIMDKEMPERDGVSTTKKIREMEVKSMTVGVTSADNEEERRAFMEAGLNHCLAKP 120
DB 61 SFDLIIMDKEMPERDGVSTTKKIREMEVKSMTVGVTSADNEEERRAFMEAGLNHCLAKP 120

QY 121 LTKDKIIPILINQMDA 136
DB 121 LTKDKIIPILINQMDA 136

RESULT 2
AA42653
ID AA42653 standard; Protein; 136 AA.
XX
AC AA42653;
DI 10-JAN-2000 (first entry)
XX
DE Brassica response regulator protein D22 putative peptide sequence.
KW Signal transduction protein; dehiscence; male sterile plant; D22 gene;
KW shatter resistance; oilseed rape; response regulator protein.
OS Brassica napus.
PN WO9949046-A1.
XX
PD 30-SEP-1999.
XX
PF 22-MAR-1999; 99WO-CB00905.
XX
PR 20-MAR-1998; 98GB-0006113.
XX
PA (BIOG-) BIOGEMMA UK LTD.
XX
PI Wyatt P, Roberts JA, Whitelaw C;
XX
DR WPI; 1999-580449/49.
DR N-PSDB; AA22977.
XX
PT A nucleic acid encoding a signal transduction protein involved in plant
PT dehiscence, useful for producing shatter resistant male sterile plants
XX
XX
XX
PS Example 2; Fig 6; 71pp; English.
XX
CC The invention provides a nucleic acid encoding a signal transduction
CC protein involved in the process of dehiscence. The nucleic acids and
CC proteins are useful for regulating or controlling dehiscence of a pod or
CC an anther in a plant, useful in the production of male sterile plants.
CC The methods, etc. may be used in production of shatter resistance or
CC shatter-delayed plants such as oilseed rape (*Brassica napus*). The present

CC sequence represents the B. napus D22 putative peptide sequence.
XX
SQ

Query Match 100.0%; Score 678; DB 20; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e-67;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATKSMGDIKIKKLNVLIVDDPLNLIHEKIIKAIGGISQTANNNGEEAVIIHRDGS 60
DB 1 MATKSMGDIKIKKLNVLIVDDPLNLIHEKIIKAIGGISQTANNNGEEAVIIHRDGS 60

QY 61 SFDLIIMDKEMPERDGVSTTKKIREMEVKSMTVGVTSADNEEERRAFMEAGLNHCLAKP 120
DB 61 SFDLIIMDKEMPERDGVSTTKKIREMEVKSMTVGVTSADNEEERRAFMEAGLNHCLAKP 120

QY 121 LTKDKIIPILINQMDA 136
DB 121 LTKDKIIPILINQMDA 136

RESULT 3
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ID AAG10549 standard; Protein; 142 AA.
XX
AC AAG10549;
DI 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8916.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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DB 61 HRDEASFDLLMDKMPERDGVSTTKKLREMKVTSIADNDEERRATMEAGLN 120
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QY 115 HCLAKPLTKDKIPLINQLMDA 136
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DB 121 HCLEKPLTKAKIFPLISHLFDA 142
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RESULT 4
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AC AAG44439;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55668.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PR 28-JUL-1999; 99US-0145951.

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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.

PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.4%; Score 538; DB 21; Length 142;
Best Local Similarity 78.9%; Pred. No. 4.7e-52;
Matches 112; Conservative 8; Mismatches 16; Indels 6; Gaps 2;

QY 1 MATKSMGDIK-----IKKL-NVLIYDDPLNLIHEKIKAIGGISQTANNGEAVII 54
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Db 1 MATKSTGGTEKTSIEVKKKLINVLIVDDDPNRRRLHEMIKIITIGGISQTAKNGEAVIL 60
    ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 55 HRDGGSEFDLILMDKEMPERDGVSTTKKLEMEYKSMIVGVTSLADNEEERRAFMEAGLN 114
    ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 HRDGEAFDLILMDKEMPERDGVSTTKKLEMKVTSIVGVTSVADQEEERKAFMEAGLN 120
    ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 HCLAKPLTKDKIILINOLMDA 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 HCLAKPLTKAKIFPLISHLFDA 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
AAY42645
ID AAY42645 standard; Protein; 142 AA.
XX AC AAY42645;
XX DT 10-TAN-2000 (first entry)
XX DE A. thaliana DZ2AT3 putative peptide sequence.
XX KW Signal transduction protein; dehiscence; male sterile plant;
    shatter resistance; oilseed rape; DZ2AT3 gene.
XX OS Arabidopsis thaliana.
XX FH Key Location/Qualifiers
FT Misc-difference 57 /note= "unknown"
FT Misc-difference 88 /note= "unknown"
XX PN WO9949046-A1.
XX 30-SEP-1999.
XX 22-MAR-1999; 99WO-GB00905.
XX 20-MAR-1998; 98GB-0006113.
XX (BIOG-) BIOEMMA UK LTD.
XX Wyatt P, Roberts JA, Whitelaw C;
XX WPI; 1999-580449/49.
XX N-PSDB; AAZ22978.
XX A nucleic acid encoding a signal transduction protein involved in plant
    dehiscence, useful for producing shatter resistant male sterile plants
    -
XX Example 3; Fig 9; 7lpp; English.
XX The invention provides a nucleic acid encoding a signal transduction
    protein involved in the process of dehiscence. The nucleic acids and
    proteins are useful for regulating or controlling dehiscence of a pod or
    an anther in a plant, useful in the production of male sterile plants.
    The methods, etc. may be used in production of shatter resistance or
    shatter-delayed plants such as oilseed rape (Brassica napus). The present
    sequence represents a DZ2 A. thaliana homologue DZ2AT3 putative peptide
    sequence.
    CC
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XX SQ Sequence 142 AA;
Query Match 76.0%; Score 515; DB 20; Length 142;
Best Local Similarity 76.1%; Pred. No. 1.7e-49;
Matches 109; Conservative 8; Mismatches 20; Indels 6; Gaps 2;

QY 1 MATKSMGDIK-----IKKKL-NVLIIVDDPDLNLIHEKIIKAIGISQANNGEEAVII 54
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MATKSTGGTEKTSIEVKKKLNLVLDPLNRRLEHMIKTIKIGISQAKNGEEXVIL 60

QY 55 HRDGGSFLLIMDKEMPERDGVSTTKKLRMEVKSMIVGVTSADNEEERRAFMEAGLN 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 HRDGEASFLLIMDKEMPERDGVSTIKKLRMEKMTSMIVGVTSVADQEEERKAFMEAGLN 120

QY 115 HCLAKPLTKDKIPLINQLMDA 136
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DB 121 HCLEKPLTKAKIPLIHLFDA 142

RESULT 6
AAY42652
ID AAY42652 standard; Protein; 116 AA.
XX AC AAY42652;
XX DT 10-JAN-2000 (first entry)
XX DE Brassica response regulator protein DZ2B putative peptide sequence.
XX KW Signal transduction protein; dehiscence; male sterile plant; DZ2B gene;
    shatter resistance; oilseed rape; response regulator protein.
XX OS Brassica napus.
XX EH Key Location/Qualifiers
XX FT Misc-difference 2 /note= "unknown"
XX PN WO9949046-A1.
XX PD 30-SEP-1999.
XX PF 22-MAR-1999; 99WO-GB00905.
XX PR 20-MAR-1998; 98GB-0006113.
XX PA (BIOG-) BIOGEMMA UK LTD.
XX PI Wyatt P, Roberts JA, Whitelaw C;
XX DR WPI; 1999-580449/49.
XX DR N-PSDB; AAZ22976.
XX PT A nucleic acid encoding a signal transduction protein involved in plant
    dehiscence, useful for producing shatter resistant male sterile plants
XX PS Example 2; Fig 6; 71pp; English.
XX CC The invention provides a nucleic acid encoding a signal transduction
    protein involved in the process of dehiscence. The nucleic acids and
    CC proteins are useful for regulating or controlling dehiscence of a pod or
    CC an anchor in a plant, useful in the production of male sterile plants.
    CC The methods, etc. may be used in production of shatter resistance or
    CC shatter-delayed plants such as oilseed rape (Brassica napus). The present
    CC sequence represents the B. napus DZ2B putative peptide sequence.
XX SQ Sequence 116 AA;
Query Match 69.6%; Score 472; DB 20; Length 116;
Best Local Similarity 80.2%; Pred. No. 8.4e-45;
Matches 93; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

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QY 21 VDDPLNLIHEKIIKAIGISQANNGEEAVIIHRDGGSFLLIMDKEMPERDGVSTT 80
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DB 1 VDDPVIKRLHEIILKISIGISQAKNGEEAVNIHRDGNASFDLIMDKEMPERDGLSAT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 KKLREMEVKSMIVGVTSADNEEERRAFMEAGLNHCLAKPLTKDKIPLINQLMDA 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 KKLREMKVTSIIIGVTTADNEEERKAFMEAGLNHCLAKPLSKAKILPLINLMDA 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
AAG10550
ID AAG10550 standard; Protein; 104 AA.
XX AC AAG10550;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 8917.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
    hybridisation assay; genetic mapping; gene expression control; promoter;
    termination sequence.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
    05-MAR-1999; 99US-0123180.
    09-MAR-1999; 99US-0123548.
    23-MAR-1999; 99US-0125788.
    25-MAR-1999; 99US-0126264.
    29-MAR-1999; 99US-0126785.
    01-APR-1999; 99US-0127462.
    06-APR-1999; 99US-0128234.
    08-APR-1999; 99US-0128714.
    16-APR-1999; 99US-0129845.
    19-APR-1999; 99US-0130077.
    21-APR-1999; 99US-0130449.
    23-APR-1999; 99US-0130510.
    28-APR-1999; 99US-0130891.
    30-APR-1999; 99US-0131449.
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    06-MAY-1999; 99US-0132485.
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    11-MAY-1999; 99US-0132863.
    14-MAY-1999; 99US-0134256.
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    14-MAY-1999; 99US-0134370.
    18-MAY-1999; 99US-0134768.
    20-MAY-1999; 99US-0134941.
    21-MAY-1999; 99US-0135124.
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    27-MAY-1999; 99US-0136021.
    28-MAY-1999; 99US-0136392.
    01-JUN-1999; 99US-0136782.
    03-JUN-1999; 99US-0137222.
    04-JUN-1999; 99US-0137528.
    07-JUN-1999; 99US-0137724.
    08-JUN-1999; 99US-0138094.
    10-JUN-1999; 99US-0138540.

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1997

Db 2 IIKTIGISQAKNGEAVILHRDGEASFDLILMDKEMPERDGVSTTKKLRMKVTSIV 61
QY 94 GVTSLADNEERAEAFWEAGLNHCLAKPLTKDKIPLINOLMDA 136
DB 62 GVTSAQDEERAEAFWEAGLNHCLAKPLTKAKIFFLSHLFDA 104

RESULT 8
ID AAG44440 standard; Protein; 104 AA.
AC AAG44440;
XX AC
XX XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55669.
XX Arabidopsis thaliana
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX XX
PD 06-SEP-2000.
XX XX
PF 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 28-MAR-1999; 99US-0126785.
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PR 06-APR-1999; 99US-0128234.
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PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
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PR 06-AUG-1999; 99US-0147303.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.

RESULT 10
AAG21090
ID AAG21090 standard; Protein: 66 AA.
XX AC AAG21090;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 23519.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 08-AUG-1999; 99US-0147303.
PR 08-AUG-1999; 99US-0147416.
PR 08-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.

PR	20-AUG-1999;	99US-0149723.	ID	XX	AG21088 standard; Protein; 71 AA.
PR	20-AUG-1999;	99US-0149929.	XX	AC	AG21088;
PR	23-AUG-1999;	99US-0149902.	XX	DT	17-OCT-2000 (first entry)
PR	23-AUG-1999;	99US-0149930.	XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 23517.
PR	25-AUG-1999;	99US-0150566.	XX	KW	Protein identification; signal transduction pathway; metabolic pathway;
PR	26-AUG-1999;	99US-0150884.	XX	KW	hybridisation assay; genetic mapping; gene expression control; promoter;
PR	27-AUG-1999;	99US-0151065.	XX	OS	termination sequence.
PR	27-AUG-1999;	99US-0151066.	XX	PN	Arabidopsis thaliana.
PR	27-AUG-1999;	99US-0151080.	XX	PD	EP1033405-A2.
PR	30-AUG-1999;	99US-0151303.	XX	XX	06-SEP-2000.
PR	31-AUG-1999;	99US-0151438.	XX	XX	25-FEB-2000; 2000EP-0301439.
PR	01-SEP-1999;	99US-0151930.	XX	XX	25-FEB-1999; 99US-0121825.
PR	01-SEP-1999;	99US-0152363.	XX	XX	05-MAR-1999; 99US-0123180.
PR	10-SEP-1999;	99US-0153070.	XX	XX	23-MAR-1999; 99US-0123548.
PR	13-SEP-1999;	99US-0153758.	XX	XX	23-MAR-1999; 99US-0125788.
PR	15-SEP-1999;	99US-0154018.	XX	XX	25-MAR-1999; 99US-0126264.
PR	16-SEP-1999;	99US-0154039.	XX	XX	01-APR-1999; 99US-0126785.
PR	20-SEP-1999;	99US-0154779.	XX	XX	01-APR-1999; 99US-0127462.
PR	22-SEP-1999;	99US-0155139.	XX	XX	06-APR-1999; 99US-0128234.
PR	23-SEP-1999;	99US-0155486.	XX	XX	08-APR-1999; 99US-0128714.
PR	24-SEP-1999;	99US-0155659.	XX	XX	16-APR-1999; 99US-0129845.
PR	24-SEP-1999;	99US-0156458.	XX	XX	19-APR-1999; 99US-0130077.
PR	28-SEP-1999;	99US-0156596.	XX	XX	21-APR-1999; 99US-0130449.
PR	04-OCT-1999;	99US-0157117.	XX	XX	23-APR-1999; 99US-0130510.
PR	05-OCT-1999;	99US-0157753.	XX	XX	23-APR-1999; 99US-0130891.
PR	06-OCT-1999;	99US-0157865.	XX	XX	28-APR-1999; 99US-0131449.
PR	07-OCT-1999;	99US-0158029.	XX	XX	30-APR-1999; 99US-0132048.
PR	08-OCT-1999;	99US-0158232.	XX	XX	30-APR-1999; 99US-0132407.
PR	12-OCT-1999;	99US-0158369.	XX	XX	04-MAY-1999; 99US-0132484.
PR	13-OCT-1999;	99US-0159293.	XX	XX	05-MAY-1999; 99US-0132485.
PR	13-OCT-1999;	99US-0159294.	XX	XX	06-MAY-1999; 99US-0132486.
PR	13-OCT-1999;	99US-0159295.	XX	XX	06-MAY-1999; 99US-0132487.
PR	14-OCT-1999;	99US-0159329.	XX	XX	07-MAY-1999; 99US-0132863.
PR	14-OCT-1999;	99US-0159330.	XX	XX	11-MAY-1999; 99US-0134256.
PR	14-OCT-1999;	99US-0159331.	XX	XX	14-MAY-1999; 99US-0134218.
PR	14-OCT-1999;	99US-0159637.	XX	XX	14-MAY-1999; 99US-0134219.
PR	18-OCT-1999;	99US-0159638.	XX	XX	14-MAY-1999; 99US-0134221.
PR	21-OCT-1999;	99US-0160741.	XX	XX	18-MAY-1999; 99US-0134370.
PR	21-OCT-1999;	99US-0160767.	XX	XX	18-MAY-1999; 99US-0134768.
PR	21-OCT-1999;	99US-0160768.	XX	XX	19-MAY-1999; 99US-0134941.
PR	21-OCT-1999;	99US-0160770.	XX	XX	20-MAY-1999; 99US-0135124.
PR	21-OCT-1999;	99US-0160814.	XX	XX	21-MAY-1999; 99US-0135333.
PR	21-OCT-1999;	99US-0160815.	XX	XX	21-MAY-1999; 99US-0135629.
PR	22-OCT-1999;	99US-0160980.	XX	XX	25-MAY-1999; 99US-0136021.
PR	22-OCT-1999;	99US-0160981.	XX	XX	27-MAY-1999; 99US-0136392.
PR	23-OCT-1999;	99US-0160989.	XX	XX	28-MAY-1999; 99US-0136782.
PR	25-OCT-1999;	99US-0161404.	XX	XX	01-JUN-1999; 99US-0137222.
PR	25-OCT-1999;	99US-0161405.	XX	XX	03-JUN-1999; 99US-0137528.
PR	25-OCT-1999;	99US-0161406.	XX	XX	04-JUN-1999; 99US-0137502.
PR	26-OCT-1999;	99US-0161359.	XX	XX	07-JUN-1999; 99US-0137724.
PR	26-OCT-1999;	99US-0161360.	XX	XX	08-JUN-1999; 99US-0138094.
PR	26-OCT-1999;	99US-0161361.	XX	XX	10-JUN-1999; 99US-0138540.
PR	28-OCT-1999;	99US-0161920.	XX	XX	10-JUN-1999; 99US-0138647.
PR	28-OCT-1999;	99US-0161922.	XX	XX	14-JUN-1999; 99US-0139119.
PR	28-OCT-1999;	99US-0161993.	XX	XX	16-JUN-1999; 99US-0139452.
PR	29-OCT-1999;	99US-0162142.	XX	XX	16-JUN-1999; 99US-0139453.
PR	29-OCT-1999;	99US-0162142.	XX	XX	17-JUN-1999; 99US-0139452.
PR	29-OCT-1999;	99US-0162142.	XX	XX	18-JUN-1999; 99US-0139454.
PR	29-OCT-1999;	99US-0162142.	XX	XX	18-JUN-1999; 99US-0139455.
PR	29-OCT-1999;	99US-0162142.	XX	XX	18-JUN-1999; 99US-0139456.
PR	29-OCT-1999;	99US-0162142.	XX	XX	18-JUN-1999; 99US-0139457.
PR	29-OCT-1999;	99US-0162142.	XX	XX	18-JUN-1999; 99US-0139458.
PR	29-OCT-1999;	99US-0162142.	XX	XX	18-JUN-1999; 99US-0139459.
PR	29-OCT-1999;	99US-0162142.	XX	XX	18-JUN-1999; 99US-0139460.

Query Match 41.3%; Score 280; DB 21; Length 66;
 Best Local Similarity 84.8%; Pred. No. 1,le-23;
 Matches 56; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 71 MPEDGVSTTKLRMEYKSMIVGVTSLADNEERRAFMEAGLNHCLAKPLTKDKIIPLI 130
 Db 1 MPEDGVSTTKLRMEYKSMIVGVTSLADNEERRAFMEAGLNHCLAKPLTKDKIIPLI 60
 QY 131 NQLMDA 136
 Db 61 SHLFDA 66

PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150586.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	30-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	28-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	02-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154773.
PR	06-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155133.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155480.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0143977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	21-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	04-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147192.			
PR	05-AUG-1999;	99US-0147260.			
PR	06-AUG-1999;	99US-0147303.			
PR	06-AUG-1999;	99US-0147416.			
PR	09-AUG-1999;	99US-0147493.			
PR	09-AUG-1999;	99US-0147935.			
PR	10-AUG-1999;	99US-0148171.			
PR	11-AUG-1999;	99US-0148319.			
PR	12-AUG-1999;	99US-0148341.			
PR	13-AUG-1999;	99US-0148565.			
PR	13-AUG-1999;	99US-0148684.			
PR	16-AUG-1999;	99US-0149368.			
PR	17-AUG-1999;	99US-0149175.			
PR	18-AUG-1999;	99US-0149426.			
PR	20-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149929.			
PR	23-AUG-1999;	99US-0149902.			
Query Match					
Best Local Similarity 31.4%; Score 213; DB 21; Length 71;					
Pred. No. 3.7e-16;					
Matches 47; Conservative 3; Mismatches 8; Indels 6; Gaps 2;					
Qy	1	MATKSMGDIEK-----IKKKL-NVLIVDDPLNLIHEKIIKAIGGISQTANGGEAVII	54		
Db	1	MATKSTGGTEKYSIEVKKLNLVLIVDDPLNRRHEMIKTIIGGISQTAKNGEAVIL	60		
Qy	55	HRDG 58			
Db	61	HRDG 64			
RESULT 12					
AAB25159					
ID AAB25159 standard; Protein: 261 AA.					
XX					
AC AAB25159;					

XX 27-NOV-2000 (first entry)
DT Pinus radiata cell signalling involved protein SEQ ID NO:127.
DE
DE Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
KW plant cell signalling; modulation; transgenic plant; pathogen; growth;
KW environmental change; development; cell proliferation; differentiation;
KW elongation; survival; disease resistance; nutrient metabolism.
KW
OS Pinus radiata.
OS
PN WO200042171-A1.
PN
XX 20-JUL-2000.
PD
XX 11-JAN-2000; 2000WO-US00724.
PF
XX 12-JAN-1999; 99US-0228986.
PR
PR 01-NOV-1999; 99US-0162866.
PR
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
PA Strabala TJ, Nieuwenhuizen NJ;
PI
PI WPI: 2000-476052/41.
DR
DR Isolated polynucleotide encoding a polypeptide involved in cell
XX signaling used for generating transgenic plants with modified responses
XX to external signals -
XX
XX Claim 3; Page 104-105; 527pp; English.
PS
XX AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
XX and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
XX pine (Pinus radiata) also known as Monterey pine). The protein sequences
XX are involved in cell signalling. The polynucleotide and protein
XX sequences can be used to modify the response of plant cells to external
XX signals e.g. environmental changes or pathogens during the growth and
XX development of a plant. They can be used to modify cell proliferation,
XX differentiation, elongation and survival, resistance to disease and
XX nutrient metabolism. Examples of modifications which can be produced are
XX altered fruit ripening and senescence of leaves and flowers e.g. to
XX delay senescence and prolong the life of cut flowers or enhance
XX senescence of reproductive organs to engineer sterile plants. Other
XX modifications can be used to delay senescence in selected cell types or
XX organs providing fruit and vegetables which have a longer shelf life
XX between harvest and consumption, or to decrease branching frequency in
XX forest tree species giving long stretches of valuable knot-free clear
XX wood which can be used in solid timber furniture and veneers.
XX
XX Sequence 261 AA;
SQ
Query Match 29.8%; Score 202; DB 21; Length 261;
Best Local Similarity 36.5%; Pred. No. 3.7e-14;
Matches 42; Conservative 34; Mismatches 37; Indels 2; Gaps 2;
QY 18 VLIVDDPLNLIITHEKIIKAIGGISOTANNGEAVIIHRDGGSSFDLILMDKEMPERDGV 77
Db 137 ILIVDDTQINRIIFGRVLOSILNYCEAENGKAVDYFKQ-GRTYDVLMDKEMPVMDGH 195
QY 78 STTKKLEMEVKSMIVGVTSLADNEERAFNAGLNHCLAKPLKDKIIPLNQ 132
Db 196 EATFQLRSMGVKTPIVALTAN-TLQSDKDLFFEAGVDYFQSPKSLRDLVLQDLQ 249
RESULT 13
ID AAY42644
XX AAY42644 standard; Protein; 67 AA.
AC
XX AAY42644;
XX 10-JAN-2000 (first entry)
DT

XX Brassica napus DZ2B partial fragment.
DE
DE Signal transduction protein; dehiscence; male sterile plant; DZ2B gene;
KW shatter resistance; oilseed rape; response regulator protein.
KW
OS Brassica napus.
OS
PN WO9949046-A1.
PN
XX 30-SEP-1999.
PD
XX 22-MAR-1999; 99WO-GB009005.
PF
XX 20-MAR-1998; 98GB-0006113.
PR
XX (BIOG-) BIOGEMMA UK LTD.
PA
XX Wyatt P, Roberts JA, Whitelaw C;
PI
XX WPI: 1999-580449/49.
DR
DR N-PSDB; AAZ22975.
DR
XX A nucleic acid encoding a signal transduction protein involved in plant
XX dehiscence, useful for producing shatter resistant male sterile plants
XX -
XX Example 2; Fig 5; 71pp; English.
PS
XX The invention provides a nucleic acid encoding a signal transduction
XX protein involved in the process of dehiscence. The nucleic acids and
XX proteins are useful for regulating or controlling dehiscence of a pod or
XX an anther in a plant, useful in the production of male sterile plants.
XX The methods, etc. may be used in the production of shatter resistance or
XX shatter-delayed plants such as oilseed rape (Brassica napus). The present
XX sequence represents the partial fragment of B. napus DZ2B protein.
XX
XX Sequence 67 AA;
SQ
Query Match 28.4%; Score 192.5; DB 20; Length 67;
Best Local Similarity 65.7%; Pred. No. 6.7e-14;
Matches 44; Conservative 6; Mismatches 10; Indels 7; Gaps 2;
QY 1 MAT--KSMGDIETK-----IKKKLNVLIVDDPLNLIITHEKIIKAIGGISOTANNGEAVI 53
Db 1 MATTSTGDIKKTKRSVEVKKLNVLIVDDTIVIRKLHENIKRSIGGISOTAKNGEAVN 60
QY 54 IHRDGG 60
Db 61 IHRDGN 67
RESULT 14
ID ABG70785
XX ABG70785 standard; Protein; 118 AA.
AC
XX ABG70785;
XX 09-DEC-2002 (first entry)
DT
XX E. coli RscC receiver region of histidine kinase.
DE
XX RscC; antagonist; agonist; cytokinin receptor;
KW receptor; signal transduction; histidine kinase; hormone; cell division;
KW cell differentiation; agriculture; growth regulator; harvest.
XX
XX Escherichia coli.
OS
XX EPI241182-A2.
PN
XX 18-SEP-2002.
PD
XX 13-MAR-2002; 2002EP-0005749.
PF

XX 15-MAR-2001; 2001JP-0073812.
PR 29-JUN-2001; 2001JP-0198639.
PR 29-JUN-2001; 2001JP-0198640.
XX (SUMO) SUMITOMO CHEM CO LTD.
XX
XX Kakimoto T, Higuchi M, Inoue T;
XX WPI; 2002-693041/75.
XX
XX Analyzing agonist or antagonist activity of a substance for use as a
PT plant growth regulator, comprises measuring intracellular signal
PT transduction from a cytokinin receptor expressed in a cell contacted
PT with the test substance.
XX
XX Disclosure; Page 42; 47pp; English.
XX
XX The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
CC presented is the E. coli receiver region of histidine kinase which can
CC transmit signals to the cytokinin receptor.
XX
XX Sequence 118 AA;
SQ
Query Match 25.3%; Score 171.5; DB 23; Length 118;
Best Local Similarity 33.9%; Pred. No. 3.2e-11;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;
QY 18 VLIVDDPLNLIITHEKIIKAIGISQTANNGEAVTIHRDGGSSFDLILMDKEMPERDV 77
Db 6 ILVDDHPINRLLADQLGSLGYQCKTANDYDALNLV--SKNHTDIVLSDVNMENMDGY 63
QY 78 STTKKLEMEVKSMIVGVTSLADNEERAFMEAGLNHCLAKPLTKDKI 126
Db 64 RLTORIRQLGLTLFVIGVTANALAEKQRC-LESGMDSCLSKRPVTLDWI 111
RESULT 15
AAO26983
ID ARO26983 standard; Protein; 471 AA.
XX
XX AAO26983;
XX
XX 10-MAY-2003 (first entry)
XX Pseudomonas aeruginosa PvrR related protein, SEQ ID No 4.
XX Antibacterial; PvrR; variant Pseudomonas; microorganism; gram negative;
KW phenotype-mediated antibiotic-resistance; gram-positive;
KW bacterial infection.
XX
XX Pseudomonas aeruginosa.
OS
XX WO2003004691-A2.
PN
XX 16-JAN-2003.
PD

XX 05-JUL-2002; 2002WO-US23242.
PF
XX 06-JUL-2001; 2001US-303286P.
PR 16-APR-2002; 2002US-37233P.
XX
XX (GEO) GEN HOSPITAL CORP.
XX Ausubel FM, Drenkard E;
XX WPI; 2003-221608/21.
DR N-PSDB; AAL55304.
XX
XX New isolated pvrR polypeptide and polynucleotide that regulates
PT bacterial biofilm formation, useful for the diagnosis, prevention and
PT treatment of gram-negative or gram-positive bacterial infection.
XX
XX Disclosure; Fig 5E; 185pp; English.
XX
XX The invention relates to a novel isolated polypeptide comprising a pvrR
CC (variant Pseudomonas) amino acid sequence having at least 50 % identity
CC to a 399 residue amino acid sequence, given in the specification, where
CC expression of the polypeptide, in a microorganism, affects phenotype-
CC mediated antibiotic-resistance in the microorganism. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and treatment of gram negative or gram-positive bacterial
CC infection. This sequence represents a Pseudomonas protein used in the
CC exemplification of the invention.
XX
XX Sequence 471 AA;
SQ
Query Match 23.1%; Score 156.5; DB 24; Length 471;
Best Local Similarity 35.8%; Pred. No. 9.9e-09;
Matches 38; Conservative 22; Mismatches 43; Indels 3; Gaps 3;
QY 16 LNVLVDDPLNLIITHEKIIKAIGISQTANNGEAVTIHRDGGSSFDLILMDKEMPERD 75
Db 352 LRVVVVEDNAINQLILRQMEALGCVSVELLDGREA-LLHCQ-TACFDVVLTDINMPNMN 409
QY 76 GVSTTKKLEMEVKSMIVGVTSLADNEERAFMEAGLNHCLAKPL 121
Db 410 GYELTAELRRQGFROPFIIGATANAMREERERC-MSAGMNDCLVKPV 454
Search completed: August 14, 2003, 16:50:31
Job time : 84 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2003, 15:46:47 ; Search time 29 seconds
(without alignments)
198.423 Million cell updates/sec

Title: US-09-646-679-15
Perfect score: 678
Sequence: 1 MATKSMGDIKIKKLNVL.....LAKPLTKDKIPLINQLMDA 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A-COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B-COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A-COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B-COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202	29.8	261	4	US-09-228-986-127
2	152.5	22.5	946	4	US-09-328-352-7973
3	150	22.1	1014	4	US-09-252-991A-31338
4	148	21.8	947	4	US-09-252-991A-29359
5	147	21.7	1627	4	US-09-252-991A-20395
6	145	21.4	1220	2	US-08-843-530B-36
7	144	21.2	162	2	US-09-252-991A-17557
8	139.5	20.6	1281	2	US-08-843-530B-6
9	139.5	20.6	1298	2	US-08-843-530B-2
10	139.5	20.6	1298	2	US-08-843-530B-34
11	139.5	20.6	1298	2	US-08-843-530B-3
12	139.5	20.6	1441	4	US-09-252-991A-28143
13	138.5	20.4	234	4	US-09-634-238-220
14	135.5	20.0	760	4	US-09-252-991A-25928
15	135.5	20.0	860	4	US-09-252-991A-26112
16	133.5	19.7	918	2	US-08-843-530B-35
17	131	19.3	764	4	US-09-252-991A-18607
18	131	19.3	1036	4	US-09-252-991A-27075
19	130	19.2	1081	2	US-08-843-530B-18
20	130	19.2	1117	2	US-08-843-530B-33
21	127	18.7	506	4	US-09-252-991A-18168
22	125	18.4	227	4	US-09-107-532A-6769
23	124.5	18.4	133	4	US-09-328-352-5134
24	124	18.3	971	3	US-09-112-450-2
25	124	18.3	971	3	US-09-419-291A-2
26	124	18.3	2471	3	US-09-112-450-4
27	124	18.3	2471	4	US-09-419-291A-4

28	122.5	18.1	265	4	US-09-328-352-6073	Sequence 6073, Ap
29	122	18.0	311	4	US-09-328-352-991A-22932	Sequence 22932, A
30	120.5	17.8	811	4	US-09-252-991A-22216	Sequence 22216, A
31	119	17.6	484	4	US-09-252-991A-31677	Sequence 31677, A
32	117	17.3	320	4	US-09-328-352-6809	Sequence 6809, Ap
33	115.5	17.0	331	4	US-09-252-991A-23765	Sequence 23765, A
34	115	17.0	762	4	US-09-228-986-114	Sequence 114, App
35	113	16.7	302	4	US-09-252-991A-29564	Sequence 29564, A
36	112.5	16.6	129	4	US-09-252-991A-16981	Sequence 16981, A
37	112.5	16.6	639	4	US-09-252-991A-17904	Sequence 17904, A
38	111.5	16.4	212	4	US-09-107-532A-6859	Sequence 6859, Ap
39	111.5	16.4	234	4	US-09-107-532A-6746	Sequence 6746, Ap
40	110.5	16.3	256	4	US-09-328-352-5430	Sequence 5430, Ap
41	110	16.2	599	4	US-09-228-986-117	Sequence 117, App
42	109	16.1	245	4	US-09-134-001C-3779	Sequence 3779, App
43	109	16.1	257	4	US-09-328-352-7397	Sequence 7397, Ap
44	108.5	16.0	246	4	US-09-107-532A-5040	Sequence 5040, Ap
45	108.5	16.0	250	4	US-09-634-238-221	Sequence 221, App

ALIGNMENTS

RESULT 1
US-09-228-986-127
; Sequence 127, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 127
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-127

Query Match 29.8%; Score 202; DB 4; Length 261;
Best Local Similarity 36.5%; Pred. No. 7e-16;
Matches 42; Conservative 34; Mismatches 37; Indels 2; Gaps 2;
QY 18 VLIVDDPLNLIHKKIKAIGGISQTANNGEEAVIHRDGGSSFDLILMKEMPERDGV 77
Db 137 ILLVDTQINRIIFGRVLQSLNLYCEEAEKGVADYFKQ-GRTYDLVLMKEMPVMDGH 195
QY 78 STTKLREVEKSMIVGVTSLADNEERRAEAGLNHCLAKPLTKKIIPLNQ 132
Db 196 EATQRLSRMGVATPIVALTA-NTLQSDKDLFEAGVDDFQSKPLSRDLVQLLDO 249

RESULT 2
US-09-328-352-7973
; Sequence 7973, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Berton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7973
; LENGTH: 946
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7973


```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,530B
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1298 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-843-530B-4

Query Match          20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

QY      2 ATKSMGDIKKKLNVLVDDPLNLIHKIIKAIGGISQTANNGEAV-IHRDGGGS 60
       ||| | : : : : : : : : : : : : : : : : : : : : : : :
Db      1075 ATPSLAD---NTSFPIILAEONTNQRLAVKILEKHVVTVYVGNEEAVEAKVR--X 1128
       ||| | : : : : : : : : : : : : : : : : : : : : : : :

QY      61 SFDLIDMKEMPERDGVSSTTKKLREME-----VKSMIVGVTSIADNEETERRAFMEAGLNH 115
       ||| | : : : : : : : : : : : : : : : : : : : : : : :
Db      1129 KFDVILDVMOPMGFGFEATKIREVERSLUGSQRPFIALLTAHA-XMGDRKCIQAQMDE 1187
       ||| | : : : : : : : : : : : : : : : : : : : : : : :

QY      116 CLAKPLTKDKRIELI 130
       ||| | : : : : :
Db      1188 YLSKPLOQNHLIQTI 1202
       ||| | : : : : :

RESULT 11
US-08-843-530B-34
; Sequence 34 Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selltreinnikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; APPLICANT: Simon, Melvin I.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,530B
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELECOMMUNICATION INFORMATION:

```


Result No.	Score	Query Match	Length	DB	ID	Description
1	202	23.8	261	15	US-10-101-464A-127	Sequence 127, Appli
2	171.5	25.3	118	10	US-09-518-508-8	Sequence 8, Appli
3	150	22.1	622	10	US-09-601-368-328	Sequence 328, Appli
4	146	21.4	1018	15	US-10-101-464A-909	Sequence 909, Appli
5	145	21.4	1220	10	US-09-601-368-332	Sequence 332, Appli
6	143.5	21.2	712	10	US-09-601-368-366	Sequence 366, Appli
7	137.5	20.3	974	15	US-10-126-120-2	Sequence 2, Appli
8	137	20.2	125	10	US-09-518-508-7	Sequence 7, Appli
9	132	19.5	1829	15	US-10-156-761-10049	Sequence 10049, A
10	128	18.9	1081	10	US-09-424-951-4	Sequence 4, Appli
11	127.5	18.8	2150	14	US-10-135-322-17	Sequence 17, Appli
12	126.5	18.7	227	9	US-09-815-242-11131	Sequence 11131, A
13	126	18.6	203	15	US-10-156-761-12532	Sequence 12532, A
14	125.5	18.5	227	15	US-10-156-761-9975	Sequence 9975, Ap
15	124.5	18.4	232	9	US-09-815-242-13783	Sequence 13783, A


```
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match 21.4%; Score 145; DB 10; Length 1220;
Best Local Similarity 29.0%; Pred. No. 6.6e-07;
Matches 40; Conservative 40; Mismatches 44; Indels 14; Gaps 6;

QY 8 DIEIKKKLNVLIVDDPLNLIHEKIIKAIGGIS--QTANNGEEA---VIIHRDGG 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1080 DDDKNETSKVLIVEDNHNV-----QEVIKRLNLEGIEINELACDGOEAFKVKELTSGK 1135
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 SFDLLIMDKEMPERDGVSTTKKL-REMEVKSIMVGVTSIADNEEERAFMEAGLNHCLA 118
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1136 ENYNMIFMDVQMPKVDGLLSTMRIRDLGYTSPVIALTAFADDSNIKEC-LESGWNGFLS 1194
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 KPLTKDKIIPNLQNLMDA 136
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1195 KPIKRPKLTILTERCAA 1212
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-09-801-368-366
; Sequence 366, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 366
; LENGTH: 712
; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-366

Query Match 21.2%; Score 143.5; DB 10; Length 712;
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42; Indels 31; Gaps 3;

QY 10 EKIKKKLNVLIVDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLLIMDK 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 498 EKVPFKINVLIVEDNVINQAILGFLRKHKISYKLAKNQGEAVNIWKEGG--LHLIFMDL 555
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 EMFERDGVSTTKKLREMEVKS-----MIVGVTSIADN 101
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 556 QLPVLSGIEAAKQIDFEKQNGIGIOKLNNSHNSLEKGTSKRFSQAPVIVALTASNSQ 615
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 102 BEERRAFMEAGLNHCLAKPL 121
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 616 MDKRRKALL-SGNDYLTTPKV 634
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Sakakibara, Hitoshi
; APPLICANT: Takel, Kentaro
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FAC
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match 20.3%; Score 137.5; DB 15; Length 974;
Best Local Similarity 24.6%; Pred. No. 3.2e-06;
Matches 35; Conservative 32; Mismatches 46; Indels 29; Gaps 3;

QY 17 NVLIVDDDDPLNLIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLLIMDKEMP 72
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 830 NILVDDDNKVNLRVAAAALKYGANVSCVSGKDAISLLQPPHR-----FDACFMDVQMP 884
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 ERDGVSTTKKLREMEVKSIMVGVTSIADNEEBERRA-----FWEAG 112
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 885 EMDGFEATGQIQOMELKANEERKNKLASIEGSTTAEYHLPVLAMTADYIQATYEECIKSG 944
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 LNHKLAKPLTKDKIIPNLQNL 134
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 945 MDGYVSKPFDDEQLYQAVSRV 966
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-918-508-7
; Sequence 7, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-918-508-7

Query Match      20.2%; Score 137; DB 10; Length 125;
Best Local Similarity 29.4%; Pred. No. 2.1e-07;
Matches 37; Conservative 38; Mismatches 37; Indels 14; Gaps 6;

QY 16 LNVLIIVDDPLNLIHKKIIEKIIKA---IGGIS--QTANNGEA---VIIHRDGGSSFDLILM 67
DB 4 VKILVVEDNHVN---QEVIKMLNLEGIEIENIACDGOEAFDKVKELTSKGENYMFIM 59

QY 68 DKEMPERDGVSTIKKL-REMEVKSIMVGVTSIADNEEERRAFMEAGLNHCLAKPLTKDKI 126
DB 60 DVQPKVDGLLSTKMRIRDLGYTSPIVALTAFAADDSNIKEC-LESGMGLFSKPKRPKL 118

QY 127 IPLINQ 132
DB 119 KTLITE 124

RESULT 9
US-10-156-761-10049
; Sequence 10049, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10049
; LENGTH: 1829
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10049

Query Match      19.5%; Score 132; DB 15; Length 1829;
Best Local Similarity 31.5%; Pred. No. 3.1e-05;
Matches 39; Conservative 24; Mismatches 51; Indels 10; Gaps 4;

QY 18 LVIVDDPLNLIHKKIIEKIIKAIGGISQTANNGEAVII---HRDGGSSFDLILMDKEMPER 74
DB 1710 LVIVDDIRNVFALTSVLEQHSVLVYAENGREGIEVLEQDD---VTVVLMIDIMPEM 1765

QY 75 DGVSTTKKIREME--VKSMIVGVTSIADNEEERRAFMEAGLNHCLAKPLTKDKIPLINQ 132
DB 1766 DGVATTATIRMPQFAGLPIIALTAKAMKGDREKA-IESGASDYVTKPVPDPHLLTYMEQ 1824

QY 133 LMDA 136
DB 1825 WMRA 1828

RESULT 10
US-09-424-951-4
; Sequence 4, Application US/09424951
; Patent No. US20020137034A1
```

```

; GENERAL INFORMATION:
; APPLICANT: SRIKANTHA, THIYAGARAJAN
; APPLICANT: SOLL, DAVID R.
; TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE,
; FILE REFERENCE: 087714/0113
; CURRENT APPLICATION NUMBER: US/09/424,951
; CURRENT FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: PCT/US98/11658
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,914
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1081
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-424-951-4

Query Match      18.9%; Score 128; DB 10; Length 1081;
Best Local Similarity 28.3%; Pred. No. 4e-05;
Matches 43; Conservative 31; Mismatches 48; Indels 30; Gaps 7;

QY 5 SMGDIERIKKKLVLIYVDDPLNLIHKKIIEKIIKAIGGISQTANNGEAV-IIHRDGGSSFD 63
DB 865 SQNSDESRYVK--ILLAEDNLVNQKLAVRILEKQGHVLEWENGLEAYEAKR---NKYD 919

QY 64 LILMDKEMPERDGVSTTKKLREMEVKS-----MIVGVTS---LADNEEERRAFME 110
DB 920 VVLMVDQVPVWGSGFEATEKIRQEKSNPIDSITFTPIALTAAHMLGDREKS---LA 975

QY 111 AGLNHCLAKPL-----TKDKIPLINQMD 135
DB 976 KGMDYVSKPLKPKLLMQTIKKKCIHNINQLKE 1007

RESULT 11
US-10-135-322-17
; Sequence 17, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 2150
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-17

Query Match      18.8%; Score 127.5; DB 14; Length 2150;
Best Local Similarity 32.5%; Pred. No. 0.00012;
Matches 37; Conservative 20; Mismatches 50; Indels 7; Gaps 3;

QY 13 KKKLVLIYVDDPLNLIHKKIIEKIIKAIGGISQTANNGEAVIIHRDGGSSFDLILMDKEMP 72
DB 2024 RKK--ALIYEDNLRKKVLAQLFKKIDWTISFAENGREA--LKEITGERCFDIVMDCOMP 2080

QY 73 ERDGVSTTK-----KLREMEVKSIMVGVTSIADNEEERRAFMEAGLNHCLAKPLT 122
DB 2081 VLDGFQTTIIRSKERENNNKRMNIVALSGSSSSSFVQDCLDSGMDSFMGPKIT 2134
```

```

RESULT 12
US-09-815-242-11131
; Sequence 11131, Application US/09815242
; Patent No. US20020061369A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11131
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11131

Query Match      18.7%; Score 126.5; DB 9; Length 227;
Best Local Similarity 28.1%; Pred. No. 6.7e-06;
Matches 34; Conservative 30; Mismatches 48; Indels 5; Gaps 2;

QY 18 VLVVDDPLNLIHKEIKAGGISQ--TANNGEAVIIHRDGGSSFDLIIMDKEMPERGV 77
Db 4 LLLVDDDLTELTSTLLELEGEDVETANNGLEAL---QKLNESYKLVLLDVMKPLNGI 60

QY 78 STTKKLRMEVKSIVGVTSIADNEERRAFMEAGLNHCLAKPLTKDKIPLINOLM 134
Db 61 ETLKEIR--KVSNPVVMALTARGEDIDRVILGELGADDCLPKPFNDRELIARIKAIL 115

RESULT 13
US-10-156-761-12532
; Sequence 12532, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9975
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12532

Query Match      18.5%; Score 125.5; DB 15; Length 227;
Best Local Similarity 29.2%; Pred. No. 8.6e-06;
Matches 38; Conservative 28; Mismatches 53; Indels 11; Gaps 5;

QY 10 EKIKKLNVLIVDDDDPLNLIHKEIKAGISQ--TANNGEAVIIHRDGGSSFDL 64
Db 4 BESRPARVAVADD---QTVVREGIVMLGLLPGIEVVGAGDGHEAVKLVAE--LNPDV 58

QY 65 ILMDKEMPERDGVSTTKKLRMEVKSIVGVTSIADNEERRAFMEAGLNHCLAKPLTKD 124
Db 59 VLMDLRMPRCDGVEATRRIRAEHPGTQVVVLTYYADESLFPA--LRAGARGYLTKDAGD 117

QY 125 KIPLINOLM 134
Db 118 EIVRAVESVL 127

RESULT 15
US-09-815-242-13783
; Sequence 13783, Application US/09815242

```

```

; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12532
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12532

Query Match      18.6%; Score 126; DB 15; Length 203;
Best Local Similarity 29.5%; Pred. No. 6.5e-06;
Matches 36; Conservative 20; Mismatches 46; Indels 20; Gaps 3;

QY 17 NVLIVDDPLNLIHKEIKAGGISQ--TANNGEAVIIHRDGGSSFDLIIMDKEMPER 74
Db 3 SVLVCDSDPLAREALRRVATVPGVERVTTAANGEE--VIRWAGADRSDLIIMDVMPL 60

QY 75 DGVSTTKKLRMEVKSIVGVTSIADNEERRAFMEAGLNHCLAKPLTKD 118
Db 61 GGVTVERLLSADPGARIIMLTVAEDLDGVALAARGYLHKDASRAELRATVTTQALA 120

QY 119 KP 120
Db 121 DP 122

RESULT 14
US-10-156-761-9975
; Sequence 9975, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9975
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9975

Query Match      18.5%; Score 125.5; DB 15; Length 227;
Best Local Similarity 29.2%; Pred. No. 8.6e-06;
Matches 38; Conservative 28; Mismatches 53; Indels 11; Gaps 5;

QY 10 EKIKKLNVLIVDDDDPLNLIHKEIKAGISQ--TANNGEAVIIHRDGGSSFDL 64
Db 4 BESRPARVAVADD---QTVVREGIVMLGLLPGIEVVGAGDGHEAVKLVAE--LNPDV 58

QY 65 ILMDKEMPERDGVSTTKKLRMEVKSIVGVTSIADNEERRAFMEAGLNHCLAKPLTKD 124
Db 59 VLMDLRMPRCDGVEATRRIRAEHPGTQVVVLTYYADESLFPA--LRAGARGYLTKDAGD 117

QY 125 KIPLINOLM 134
Db 118 EIVRAVESVL 127

RESULT 15
US-09-815-242-13783
; Sequence 13783, Application US/09815242

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Thu Aug 14 17:18:19 2003

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; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Cari, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13783
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Salmonella typhi
; US-09-815-242-13783
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Query Match      18.4%; Score 124.5; DB 9; Length 232;
Best Local Similarity 28.2%; Pred. No. 1.1e-05;
Matches 33; Conservative 31; Mismatches 48; Indels 5; Gaps 2;

Qy 18 VLIYDDPLNLIHKKIIRKIGISQTANNNGEAVIHRDGGSPDLIMDKEMPERDGV 77
Db 4 ILLVDDRELTSLKELLEMEGFNLVAHDGQALELLDD---SIDLLLDVMMPEKNGI 60

Qy 78 STTKKLEMEVKSMIVGVTSIADNEERAFRAEAGLNHCLAKPLTKDKIPLINOLM 134
Db 61 DTUKALRQTHQTPVI--MLTARGNELDRVLGLELGGADLYLPKPFNDRELVAIRAIL 115
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Search completed: August 14, 2003, 16:59:18
Job time : 56 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 14, 2003, 16:46:47 ; Search time 39 Seconds
(without alignments)
335,357 Million cell updates/sec

Title: US-09-646-679-15
Perfect score: 678
Sequence: 1 MATKSMGDIKKKLNVL.....LAKPLTKDKIIPLINQLMDA 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	26.7	1969	2 T08875	histidine kinase h
2	178.5	26.3	1197	1 G55010	sensor protein evg
3	176.5	26.0	1197	2 A91035	probable sensor fo
4	176.5	26.0	1197	2 C85879	probable sensor fo
5	174	25.7	394	2 H87640	sensor histidine k
6	173.5	25.6	948	2 AD0790	sensor protein Rcs
7	171.5	25.3	933	1 BVECCC	sensor protein rcs
8	171.5	25.3	933	2 C91017	sensor for ctr cap
9	171.5	25.3	933	2 B85861	hypothetical prote
10	171.5	25.3	957	2 AD0149	two component sens
11	162.5	24.0	642	2 E87644	sensor box histid
12	162.5	24.0	778	2 AD0432	aerobic respiratio
13	159	23.5	117	2 A69487	response regulator
14	159	23.5	736	2 C82151	sensor histidine k
15	159	23.5	1645	2 AG1897	two-component hybr
16	157	23.2	900	2 B7252	sensor box histid
17	156.5	23.1	777	2 A35966	chemotaxis protein
18	155	22.9	690	2 A87580	sensor box histid
19	154.5	22.8	122	2 G69422	response regulator
20	154.5	22.8	572	2 B82198	sensor histidine k
21	153.5	22.6	713	2 A87617	sensor box histid
22	152.5	22.5	120	1 S58645	response regulator
23	152.5	22.5	120	2 G84253	chemotaxis protein
24	152.5	22.5	514	2 A87266	sensor histidine k
25	152	22.4	1014	1 S75023	sensor transducti
26	151.5	22.3	633	2 S75525	sensor transducti
27	150.5	22.2	778	2 AG0906	aerobic respiratio
28	150.5	22.2	939	2 A80032	two-component sens
29	150	22.1	622	1 A49344	cell wall assembly

30	150	22.1	992	2 A83324	probable sensor/re
31	149.5	22.1	776	1 R95CAR	aerobic respiratio
32	149.5	22.1	778	2 A91140	aerobic respiratio
33	149.5	22.1	778	2 D85985	aerobic respiratio
34	148	21.8	925	2 E83529	sensor/response re
35	147	21.7	1212	2 F83153	probable two-compo
36	145	21.4	1220	2 S48387	SLN1 protein - yea
37	144.5	21.3	560	2 E87460	sensor histidine k
38	144	21.2	857	2 C82424	sensor histidine k
39	144	21.2	919	2 E83212	probable sensor/re
40	143.5	21.2	712	2 S64828	SSK1 protein - yea
41	143	21.1	693	2 C87575	sensor histidine k
42	142.5	21.0	637	2 D87559	sensor box histid
43	142.5	21.0	918	2 AI0860	sensor protein (im
44	142	20.9	152	2 H97516	probable response
45	142	20.9	929	2 B41863	two-component regu

ALIGNMENTS

RESULT 1

T08875
histidine kinase homolog DHKB - slime mold (Dictyostelium discoideum)
N:Alternate names: Hybrid Histidine Kinase DHKB
C:Species: Dictyostelium discoideum
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-May-2000
C:Accession: T08875
R:Zinda, M.J.; Singleton, C.K.
Dev Biol 196, 171-183, 1998
A:Title: The Hybrid histidine kinase dhxB regulates score germination in Dictyostelium
A:Reference number: Z16506; MUID:98248997; PMID:9576830
A:Accession: T08875
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1969 <SIN>
A:Cross-references: EMBL:AF024654; NID:g2460282; PID:g2460283
A:Experimental source: Strain KAX3
C:Genetics:
A:Gene: dhxB
A:Introns: 790/73
C:Superfamily: response regulator homology
C:Keywords: Protein kinase; transmembrane protein
F:1841-1964/Domain: Response regulator homology <RRH>

Query Match	26.7%	Score 181;	DB 2;	Length 1969;
Best Local Similarity	35.8%;	Pred. No. 5.6e-07;		
Matches	48;	Conservative 29;	Mismatches 39;	Indels 18; Gaps 5;
QY	10	EKIKKLNVLIVDDPLNLIHEKIKAIGGISQTANNGEAAVILHRDGGSGSFOLIIMDK	69	
DB	1836	EKIEK---ILLVDENFVNKVFISKLKDSGYIFDVAHNGVEAVECVKKG--AYDLILMDC	1890	
QY	70	EMPERDGVSTTKLREMEVKSMI-----VGVTSLADNP--ERRAFVEAGLNHCL	117	
DB	1891	QMPENDGFEATTAIRELEKSNLIESPPSKHSHVIVALTANSYKDKOKCLSVGMNDFL	1950	
QY	118	AKPL-TDKIIPLI	130	
DB	1951	QPKIKTSILIQMI	1964	

RESULT 2

G55010
sensor protein evgs (EC 2.7.3.-) precursor - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C:Accession: G55010; J00221; I41200
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.,
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: G65010
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1197 <BLAT>
A:Cross-references: GB:AE000325; GB:U00096; NID:g1788709; PIDN:AACT5429.1; PID:g1788713
A:Experimental source: strain K-12, substrain MG1655
R:Utsumi, R.
A:Title: Newly identified genes involved in the signal transduction of Escherichia coli
A:Reference number: 141198; MUID:94171083; PMID:8125343
A:Accession: I41200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151, 'F', 153-241, 'PL', 244-274, 'R', 276-419, 'FE', 422-738, 'D', 740-757, 'K', 759-
A:Cross-references: GB:D14008; NID:9456162; PIDN:BAA03108.1; PID:g216554
C:Genetics:
A:Gene: evgs
C:Superfamily: evgs protein; response regulator homology
C:Keywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase;
F:687-935/Domain: sensor histidine kinase homology <SHK>
F:961-1070/Domain: response regulator homology <RRH>
F:721/Binding site: phosphate (His) (covalent) #status predicted
F:1003/Binding site: phosphate (Asp) (covalent) #status predicted
Query Match 26.3%; Score 178.5; DB 1; Length 1197;
Best Local Similarity 34.4%; Pred. No. 5.1e-07;
Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;
QY 12 IKKLNVLIVDDPLNLIIHEKIIKAIGISQTANNGEAAVIIHRDGGSSFDLILMDKEM 71
Db 955 LPEKLSILIIADHPNRLLLKRLNLLGYDVEATDGVQA--LHKVSMQHYDLITDVM 1012
QY 72 PERDGVSTTKKREMEVKSMIVGVTSLADNEERAFMEAGLNHCLAKPLTKKIPLIN 131
Db 1013 PNVDGFELTRKLRQNSLPIWGLTANA-QANEREKGLSCGMNLCLEPKPLTLDVLKTHLS 1071
QY 132 QL 133
Db 1072 QL 1073
RESULT 3
A91035
Probable sensor for regulator EvgA [imported] - Escherichia coli (strain O157:H7, substr
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C:Accession: A91035
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A91035
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1197 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036672.1; PID:g13362719; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: Ecs3249
C:Superfamily: evgs protein; response regulator homology
Query Match 26.0%; Score 176.5; DB 2; Length 1197;
Best Local Similarity 34.4%; Pred. No. 7.5e-07;
Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;
QY 12 IKKLNVLIVDDPLNLIIHEKIIKAIGISQTANNGEAAVIIHRDGGSSFDLILMDKEM 71
Db 955 LPEKLSILIIADHPNRLLLKRLNLLGYDVEATDGVQA--LHKVSMQHYDLITDVM 1012
QY 72 PERDGVSTTKKREMEVKSMIVGVTSLADNEERAFMEAGLNHCLAKPLTKKIPLIN 131
Db 1013 PNVDGFELTRKLRQNSLPIWGLTANA-QANEREKGLSCGMNLCLEPKPLTLDVLKTHLS 1071
QY 132 QL 133
Db 1072 QL 1073
RESULT 5
H87640
sensor histidine kinase/response regulator [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87640
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete genome sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87640
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <STO>
A:Cross-references: GB:AE005673; NID:g13424832; PIDN:AAK25124.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3162
Query Match 25.7%; Score 174; DB 2; Length 394;
Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;

QY 12 IKKLNVLIVDDPLNLIIHEKIIKAIGISQTANNGEAAVIIHRDGGSSFDLILMDKEM 71
Db 955 LPEKLSILIIADHPNRLLLKRLNLLGYDVEATDGVQA--LHKVSMQHYDLITDVM 1012
QY 72 PERDGVSTTKKREMEVKSMIVGVTSLADNEERAFMEAGLNHCLAKPLTKKIPLIN 131
Db 1013 PNVDGFELTRKLRQNSLPIWGLTANA-QANEREKGLSCGMNLCLEPKPLTLDVLKTHLS 1071
QY 132 QL 133
Db 1072 QL 1073
RESULT 4
C85879
Probable sensor for regulator EvgA evgs [imported] - Escherichia coli (strain O157:H7
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C85879
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C85879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1197 <STO>
A:Cross-references: GB:AE005174; NID:g12516740; PIDN:AAG57495.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: evgs
C:Superfamily: evgs protein; response regulator homology
Query Match 26.0%; Score 176.5; DB 2; Length 1197;
Best Local Similarity 34.4%; Pred. No. 7.5e-07;
Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;
QY 12 IKKLNVLIVDDPLNLIIHEKIIKAIGISQTANNGEAAVIIHRDGGSSFDLILMDKEM 71
Db 955 LPEKLSILIIADHPNRLLLKRLNLLGYDVEATDGVQA--LHKVSMQHYDLITDVM 1012
QY 72 PERDGVSTTKKREMEVKSMIVGVTSLADNEERAFMEAGLNHCLAKPLTKKIPLIN 131
Db 1013 PNVDGFELTRKLRQNSLPIWGLTANA-QANEREKGLSCGMNLCLEPKPLTLDVLKTHLS 1071
QY 132 QL 133
Db 1072 QL 1073

A:Title: RcsB and RcsC: a two-component regulator of capsule synthesis in Escherichia coli
A:Reference number: JY0068; MUID:90130299; PMID:2404948
A:Accession: JY0069
A:Molecule type: DNA
A:Residues: 1-112; IG', 115-918, 'S', 920-933 <STO>
A:Cross-references: GB:M28242; NID:g147524; PIDN:AAA24503.1; PID:g147525
A:Experimental source: strain K12
R:Jayaratne, P.; Keenleyside, W.J.; MacLachlan, P.R.; Dodgson, C.; Whitfield, C.
J. Bacteriol. 175, 5384-5394, 1993
A:Title: Characterization of rcsB and rcsC from Escherichia coli O9: K30:H12 and exam
F:811-920/Domain: response regulator #status predicted <TM2>
F:463/Binding site: phosphate (His) (covalent) #status predicted
F:859/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 25.3%; Score 171.5; DB 1; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.5e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

Qy 18 VLIVDDPLNLIIHEKIIKAIGISQTANNGEAVIHRDGGSFLLIMDKEMPERDGV 77
:||||| : : : : ||||| : : : : : : : : : :
Db 811 ILVVDHPINRLADQLGSLGYCKTANDGVDAENV--SKNHIDIVLSDVNPMDGY 868
:
Qy 78 STTKLRMEVKSMIVGTSLADNEERAFRAEAGLNHCLAKPLTKDKI 126
:
Db 869 RLQRIQLGLTLPIVGVTANALAEKQRCLSGMDSCLSKPVTLDVI 916
: :

RESULT 8
C91017
sensor for ctr capsule biosynthesis [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: C91017
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91017
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-933 <RAY>
A:Cross-references: GB:BA000007; PIDN:BA836530.1; PID:g13362576; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: EC3107
C:Superfamily: rcsC protein; response regulator homology

Query Match 25.3%; Score 171.5; DB 2; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.5e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

Qy 18 VLIVDDPLNLIIHEKIIKAIGISQTANNGEAVIHRDGGSFLLIMDKEMPERDGV 77
:||||| : : : : ||||| : : : : : : : : : :
Db 811 ILVVDHPINRLADQLGSLGYCKTANDGVDAENV--SKNHIDIVLSDVNPMDGY 868
:
Qy 78 STTKLRMEVKSMIVGTSLADNEERAFRAEAGLNHCLAKPLTKDKI 126
: ~~~~~~

Db 869 RLTORIQLGLTLPIGVITANALAEKQRC-LESGMDSCLSKPVTLDVI 916

RESULT 9

ES5861

Hypothetical protein rscC [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: E85861

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-933 <STO>

A:Cross-references: GB:AE005174; NID:g12516556; PIDN:AA57353.1; GSPDB:GN00145; UWGP:Z34

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: rscC

C:Superfamily: rscC protein; response regulator homology

Query Match 25.3%; Score 171.5; DB 2; Length 933;

Best Local Similarity 33.9%; Pred. No. 1.5e-06;

Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

Qy 18 LVIVDDPPLNLIIEKIIKAIGISQTANNGEAVIIHRDGGSSFDLIIMDKEMPERDGV 77

Db 811 ILVDDHPINRLADQLGSLGYCKTANDGVDAIENVL--SKNIDIVLSDVNPNDGY 868

Qy 78 STTKKLREMEVKSMIVGVTSLADNSEEERRAFMEAGLNHCLAKPLTKDKI 126

Db 869 RLTORIQLGLTLPIGVITANALAEKQRC-LESGMDSCLSKPVTLDVI 916

RESULT 10

AD0149

two component sensor kinase/response regulator protein RscC (EC 2.7.3.-) [imported] - Yersinia pestis

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C:Accession: AD0149

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; Genot-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Cross-references: GB:AL590842; PIDN:CAC90055.1; PID:g15979276; GSPDB:GN00175

A:Accession: AD0149

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-957 <RUR>

A:Cross-references: GB:AL590842; PIDN:CAC90055.1; PID:g15979276; GSPDB:GN00175

C:Genetics:

A:Gene: rscC

C:Superfamily: rscC protein; response regulator homology

C:Keywords: phosphotransferase

Query Match 25.3%; Score 171.5; DB 2; Length 957;

Best Local Similarity 35.1%; Pred. No. 1.5e-06;

Matches 39; Conservative 29; Mismatches 40; Indels 3; Gaps 2;

Qy 16 LNVIVDDPPLNLIIEKIIKAIGISQTANNGEAVIIHRDGGSSFDLIIMDKEMPERD 75

Db 835 LQILVDDHPINRLADQLTGLGYRTANDGLDAIENVL--NTVDVNLITDNNPND 892

Qy 76 GVSTTKKLREMEVKSMIVGVTSLADNSEEERRAFMEAGLNHCLAKPLTKDKI 126

Db 893 GYRLTERLNQNFNFIIGVTANALAEKQRC-IEAGMDCNLSKRPVTLDTL 942

RESULT 11

EB7644

sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: E87644

R:Ritterman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.B.; Haft, D.H.; Ko, N.; J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87644

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-642 <STO>

A:Cross-references: GB:AE005673; NID:g13424865; PIDN:AAK25153.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3191

Query Match 24.0%; Score 162.5; DB 2; Length 642;

Best Local Similarity 33.0%; Pred. No. 5.5e-06;

Matches 36; Conservative 28; Mismatches 40; Indels 5; Gaps 2;

Qy 16 LNVIVDDPPLNLIIEKIIKAIGISQTANNGEAVIIHRDGGSSFDLIIMDKEMPERD 75

Db 514 LHVLLVEDNATNRLIATRLMEALGARVTAEAGQGVAAARQG---FDLIIMDIQMPVMD 570

Qy 76 GVSTTKKLREMEVKSMIVGVTSLADN--EERRAFMEAGLNHCLAKPLT 122

Db 571 GVEATHIRAFNSPAGAAPILAMTANAKAHQQAASVLAAGMDGAIKAPLS 619

RESULT 12

AD0432

aerobic respiration control sensor/response regulatory protein (EC 2.7.3.-) [imported]

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C:Accession: AD0432

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; Genot-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Cross-references: GB:AL590842; PIDN:CAC92784.1; PID:g15981477; GSPDB:GN00175

A:Accession: AD0432

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-778 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92784.1; PID:g15981477; GSPDB:GN00175

C:Genetics:

A:Gene: arcB

C:Superfamily: aerobic respiration control sensor protein arcB; response regulator homology

C:Keywords: phosphotransferase

Query Match 24.0%; Score 162.5; DB 2; Length 778;

Best Local Similarity 27.0%; Pred. No. 6.8e-06;

Matches 33; Conservative 38; Mismatches 48; Indels 3; Gaps 2;

Qy 16 LNVIVDDPPLNLIIEKIIKAIGISQTANNGEAVIIHRDGGSSFDLIIMDKEMPERD 75

Db 525 LHVLLVEDIENLVIVARSVLEKLGNSVDVAMNGDALAMFNP--EDFVLVLDIQLPDMS 582

Qy 76 GVSTTKKLREMEVKSMIVGVTSLADN--EERRAFMEAGLNHCLAKPLTKDKI 134

Db 583 GLDIATQIRAEYCKQSILPLVALTANVLAKDKKEYLDAGMDVLSKPLSVLPALTAMIKQFV 642

Qy 135 DA 136

Db 643 DS 644

RESULT 13

A69487

response regulator homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Mar-2003
C:Accession: A69487
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69487
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-117 <KLE>
A:Cross-references: GB:AE000971; GB:AE000782; NID:92689294; PIDN:AA89351.1; PID:g264864
C:Superfamily: signal transduction receiver (phosphoacceptor) protein (CheY-like); respo
C:Keywords: phosphoprotein
F:4-110/Domain: response regulator homology <RRH>
F:50/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 23.5%; Score 159; DB 2; Length 117;
Best Local Similarity 28.3%; Pred. No. 1.5e-06;
Matches 36; Conservative 42; Mismatches 31; Indels 18; Gaps 5;

Qy 16 LNLVIVDD-----DPLNLIHE-KIKAIGGISQTANNGEAVIHRDGGSSFDLILMDK 69
Db 2 IKVWVDDDEIAEMRIKILMKDYKVTIE-----ASNGREAVEIYRE-ERPDIIVLMDV 51
Qy 70 EMERDGVSTTKLRMEVKSMIVGVTSLADNEERRAFMEAGLNHCLAKPTKDKIPL 129
Db 52 MWPLMNGIEATSEIKIDPDAKIVATAYASSKGEK--VIEAGADYILKKPTTRKEVEL 109
Qy 130 INQLMD 136
Db 110 IKRILNS 116

*RESULT 14

C82151 sensor histidine kinase VC1831 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82151
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82151
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-736 <HEI>
A:Cross-references: GB:AE004259; GB:AE003852; NID:9656353; PIDN:AAF94979.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1831
A:Map position: 1

Query Match 23.5%; Score 159; DB 2; Length 736;
Best Local Similarity 30.8%; Pred. No. 1.3e-05;
Matches 41; Conservative 35; Mismatches 45; Indels 12; Gaps 5;

Qy 8 DIEIKKK-----LNLVIVDDPLNLIHEKIIKAIGGISQTANNGEAVIHRDGGSSFD 63
Db 590 DVKPTKATYPLGLRVLIVEDNRTIMILEAFMRNKGPECHSVMDGVQAITALQEE--SSFD 647
Qy 64 LILMDKEMPERDGVSTTKLRME--BVKSMIVGVTSLAD-NEERRAFMEAGLNHCLAK 119
Db 648 LVLMDNMPLKDGIOATREINQLPLQAKILLFGCT--ADVFKDTRDKMLSGADDDIAR 705

Qy 120 PLTKDKIILPLNQ 132
Db 706 PIAEHLELDWALEQ 718

RESULT 15

AG1897
two-component hybrid sensor and regulator all0729 [imported] - Nostoc sp. (strain PCC
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG1897
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1897
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1645 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072686.1; PID:g17130074; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0729

Query Match 23.5%; Score 159; DB 2; Length 1645;
Best Local Similarity 27.7%; Pred. No. 3.1e-05;
Matches 39; Conservative 40; Mismatches 50; Indels 12; Gaps 3;

Qy 3 TKSNGDIEIKKKLNLVIVDDPLNLIHEKIIKAIGGISQTANNGEAVIHRDGGSSF 62
Db 1414 TRSVIGLAPQQRCLVVDVADSRLLVLLKLLSVGFVQVQEAANGQALAIWQWHP-- 1471
Qy 63 DLILMDKEMPERDGVSTTKLRMEVK-----SMIVGVTSLADNEERRAFMEAGL 113
Db 1472 QLILMDMRPIMDGYEATHFIRSAEIEHTTIPNPTIILATAA-PEEQOAMLVQGC 1530
Qy 114 NHCLAKPLTKDKIILPLNQLM 134
Db 1531 DDLINKPFSEKEILEKLNKYL 1551

Search completed: August 14, 2003, 16:51:17
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: August 14, 2003, 16:46:47 ; Search time 23 Seconds
(without alignments)
278.071 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MATKSNMGDIKKIKKLVLI.....LAKPLTKKIPLINQLMDA 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178.5	26.3	1197	1 EVGS_ECOLI	P30855 escherichia
2	176.5	26.0	1197	1 EVGS_ECO57	P58402 escherichia
3	173.5	25.6	948	1 RCSC_SALTI	Q56128 salmonella
4	172.5	25.4	948	1 RCSC_SALTY	P58562 salmonella
5	171.5	25.3	949	1 RCSC_ECOLI	P14376 escherichia
6	156.5	23.1	777	1 FRZE_MXXA	P18769 myxococcus
7	150	22.1	622	1 SKN7_YEAST	P38989 saccharomyc
8	149.5	22.1	778	1 ARCB_ECO57	P58563 escherichia
9	149.5	22.1	778	1 ARCB_ECOLI	P22763 escherichia
10	145	21.4	1220	1 SLNT_YEAST	P39928 saccharomyc
11	143.5	21.2	712	1 SSK1_YEAST	Q07084 saccharomyc
12	142	20.9	907	1 GACS_PSESY	P48027 pseudomonas
13	140.5	20.7	226	1 DCTR_BACSU	P96602 bacillus su
14	140.5	20.7	230	1 DCTR_BACSD	Q9k998 bacillus ha
15	134	19.8	119	1 CHEF_BACSU	P24072 bacillus su
16	134	19.8	1238	1 BVGS_BORPE	P16575 bordetella
17	133.5	19.7	228	1 DCTR_BACME	P39486 bacillus me
18	133.5	19.7	918	1 BARA_ECOLI	P26607 escherichia
19	132.5	19.5	131	1 YSOL_PLEBO	P51586 plectonema
20	132.5	19.5	918	1 BARA_SHIFL	P59342 shigella fl
21	132	19.5	859	1 LUXO_VIBHA	P54302 vibrio harv
22	131.5	19.4	441	1 ZRAR_SALTI	Q82333 salmonella
23	131.5	19.4	441	1 ZRAR_SALTY	P25852 salmonella
24	130	19.2	1238	1 BVGS_BORPA	P40330 bordetella
25	129.5	19.0	849	1 LUXN_VIBHA	P54301 vibrio harv
26	127.5	18.8	522	1 MCS4_SCHPO	P87323 schizosacch
27	127	18.7	1238	1 BVGS_BORBR	P26762 bordetella
28	126.5	18.7	227	1 CPXR_BORBR	P44895 haemophilus
29	125.5	18.5	443	1 ZRAR_KLEOX	Q9apd9 klebsiella
30	124	18.3	144	1 CHEY_TREPA	P96126 treponema p
31	124	18.3	539	1 PRRI_SCHPO	O14283 schizosacch
32	122.5	18.1	441	1 ZRAR_ECOLI	P14375 escherichia
33	122	18.0	248	1 ALGR_PSEAE	P26275 pseudomonas

RESULT 1

ID	EVGS_ECOLI	STANDARD	PRT	1197 AA
AC	P30855; P77644; Q9RF36; Q9RF37;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Sensor protein evgs precursor (EC 2.7.3.-).			
GN	EVGS OR B2370.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=94171083; PubMed=8125343;			
RA	Utsumi R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki S.,			
RA	Nakagawa H., Miwa A., Tanabe H., Noda M.;			
RT	"Newly identified genes involved in the signal transduction of			
RT	Escherichia coli K-12.";			
RL	Gene 140:73-77(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=93173621; PubMed=1289796;			
RA	Utsumi R., Katayama S., Ikeda M., Igaki S., Nakagawa H., Miwa A.,			
RA	Taniguchi M., Noda M.;			
RT	"Cloning and sequence analysis of the evgAS genes involved in signal			
RT	transduction of Escherichia coli K-12.";			
RL	Nucleic Acids Symp. Ser. 27:149-150(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A. (VARIANTS EVGS1 AND EVGS4).			
RC	STRAIN=K12;			
RX	MEDLINE=20378313; PubMed=10923791;			
RA	Kato A., Ohnishi H., Yamamoto K., Furuta E., Tanabe H., Utsumi R.;			
RT	"Transcription of emrKY is regulated by the EvgA-Evgs two-component			
RT	system in Escherichia coli K-12.";			
RL	Biosci. Biotechnol. Biochem. 64:1203-1209(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1453-1474(1997).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=97349980; PubMed=9205837;			
RA	Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Tsuno K.,			
RA	Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,			
RA	Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,			

ALIGNMENTS

34	121.5	17.9	441	1 ZRAR_ECO57	Q8x613 escherichia
35	119.5	17.6	216	1 NARL_ECOLI	P10957 escherichia
36	119.5	17.6	226	1 CITT_BACSU	Q34534 bacillus su
37	119.5	17.6	231	1 CTRA_CAUCR	Q45994 caulobacter
38	118.5	17.5	232	1 CPXR_ECOLI	P16244 escherichia
39	117	17.3	225	1 CSCR_ALCEU	Q44006 alcaligenes
40	115.5	17.0	677	1 RPFC_XANCP	P49246 xanthomonas
41	115	17.0	120	1 CHEY_THEMA	Q56312 thermotoga
42	115	17.0	243	1 YC27_PORFU	P31358 porphyra pu
43	112.5	16.6	121	1 PILH_PSEAE	P43501 pseudomonas
44	112.5	16.6	461	1 ATOC_ECOLI	Q06065 escherichia
45	111.5	16.4	254	1 YC27_GUITH	O78428 guillardia

RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horiuchi T.;
 FT "Construction of a contiguous 874-kb sequence of the *Escherichia coli*
 RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
 RL analysis of its sequence features.";
 RN DNA Res. 4:91-113(1997).
 [6]
 RP CHARACTERIZATION.
 RX MEDLINE=98194702; PubMed=9535079;
 RA Perraud A., L., Kimmel B., Weiss V., Gross R.;
 RA "Specificity of the evgAs and EvgS phosphorelay is mediated by the
 RT C-terminal Hpt domains of the sensor proteins.";
 RL Mol. Microbiol. 27:875-887(1998).
 CC -|- FUNCTION: Member of the two-component regulatory system evgS/evgA.
 CC Phosphorylates evgA via a four-step phosphorelay in response to
 CC environmental signals.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Probable).
 CC -|- PM: Activation requires a sequential transfer of a phosphate
 CC group from a His in the primary transmitter domain, to an Asp in
 CC the receiver domain and to a His in the secondary transmitter
 CC domain.
 CC -|- SIMILARITY: Contains 1 histidine kinase domain.
 CC -|- SIMILARITY: Contains 1 HPT domain.
 CC -|- SIMILARITY: Contains 1 response regulatory domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D14008; BAA03108.1; -;
 DR EMBL: AF201840; AAF1563.1; -;
 DR EMBL: AF201841; AAF1564.1; -;
 DR EMBL: AE000325; AAC75429.1; -;
 DR EMBL: D90867; BAA16241.1; -;
 DR PIR: G65010; G65010.
 DR HSP: P06143; IUDR.
 DR EcoGene: EG11610; evgs.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR003661; His_kinA.
 DR InterPro: IPR005467; His_kinase.
 DR InterPro: IPR002570; Hpt.
 DR InterPro: IPR001789; Response_reg.
 DR InterPro: IPR001311; SBP/glu_receptor.
 DR InterPro: IPR001638; SBP_bac_3.
 DR Pfam: PF02518; HATPase_C; 1.
 DR Pfam: PF00512; HiskA; 1.
 DR Pfam: PF00072; response_reg; 1.
 DR Pfam: PF00497; SBP_bac_3; 1.
 DR PRINTS: PR00344; BCTR1SENSOR.
 DR ProDom: PD000039; Response_reg; 1.
 DR SMART: SM00387; HATPase_C; 1.
 DR SMART: SM00388; HiskA; 1.
 DR SMART: SM00073; Hpt; 1.
 DR SMART: SM00052; PBPb; 2.
 DR SMART: SM00448; REC; 1.
 DR SMART: PS0109; HIS_KIN; 1.
 DR PROSITE: PS0894; HPT; 1.
 DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Transferrase; Kinase; Phosphorylation;
 KW Transmembrane; Inner membrane; Signal; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 1197
 FT DOMAIN 22 325
 FT TRANSMEM 326 346
 FT DOMAIN 347 537
 FT TRANSMEM 538 558
 FT POTENTIAL.

FT DOMAIN 559 1197 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 718 938 HISTIDINE KINASE.
 FT DOMAIN 960 1074 RESPONSE REGULATORY.
 FT HPT.
 FT MOD_RES 721 721 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1009 1009 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1137 1137 PHOSPHORYLATION (BY SIMILARITY).
 FT VARIANT 577 577 F -> S (IN EVGS1; CONSTITUTIVELY ACTIVE).
 FT VARIANT 701 701 E -> G (IN EVGS4; CONSTITUTIVELY ACTIVE).
 FT CONFLICT 152 152 L -> F (IN REF. 1 AND 2).
 FT CONFLICT 242 243 W -> R (IN REF. 1 AND 2).
 FT CONFLICT 275 275 SQ -> FE (IN REF. 1 AND 2).
 FT CONFLICT 420 421 G -> D (IN REF. 1 AND 2).
 FT CONFLICT 739 739 G -> K (IN REF. 1 AND 2).
 FT CONFLICT 758 758 L -> V (IN REF. 1 AND 2).
 FT CONFLICT 761 761 S -> L (IN REF. 1 AND 2).
 FT CONFLICT 877 877 R -> H (IN REF. 1 AND 2).
 FT CONFLICT 1045 1045 H -> Y (IN REF. 1 AND 2).
 FT CONFLICT 1074 1074 H -> Y (IN REF. 1 AND 2).
 SQ SEQUENCE 1197 AA; 134742 MW; E8E1DE0F797B1278 CRC64;
 Query Match 26.3%; Score 178.5; DB 1; Length 1197;
 Best Local Similarity 34.4%; Pred No. 2.9e-07;
 Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;
 QY 12 IKKLVIVDDPLNLIHEKIKKIGISQQTANNGEEAVIHRDGGSPFDJILMDKEM 71
 Db 955 LPEKLSILADDPHTNRLKLLKQLNLLGYDDEATDGVQA--LHKVSMQHVDDLLITDVM 1012
 QY 72 PERDGVSTTKKREMEVKSMIVGTSLADNEEERAFMEAGINHCAPKPTKDIIPLIN 131
 Db 1013 PNWDGELTRKLRQNSSLPINGLTANA-QANEREKGLSCGMNLCFLPFLDLVLKTHLS 1071
 QY 132 QL 133
 Db 1072 QL 1073
 RESULT 2
 EVGS_ECO57 STANDARD; PRT; 1197 AA.
 ID EVGS_ECO57
 AC P38402;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sensor protein evgs precursor (EC 2.7.3.-).
 GN EVGS OR 23632 OR ECS3249.
 OS *Escherichia coli* O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamous K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ocasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";

RL DNA Res. 8.11-22(2001)).

CC -!- FUNCTION: Member of the two-component regulatory system evgs/evga.

CC Phosphorylates evga via a four-step phosphorelay in response to

CC environmental signals (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

CC (Probable).

CC -!- PTM: Activation requires a sequential transfer of a phosphate

CC group from a His in the primary transmitter domain, to an Asp in

CC the receiver domain and to a His in the secondary transmitter

CC domain (By similarity).

CC -!- SIMILARITY: Contains 1 histidine kinase domain.

CC -!- SIMILARITY: Contains 1 HPT domain.

CC -!- SIMILARITY: Contains 1 response regulatory domain.

CC

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CC -----

CC EMBL; AE005468; AG57495.1; -.

CC EMBL; AP002561; BAB36672.1; -.

CC PIR; A91035; A91035.

CC PIR; C85879; C85879.

CC InterPro: IPR003594; ATPbind_Atpase.

CC InterPro: IPR004358; Bact_sens_pr_C.

CC InterPro: IPR003661; His_kinA.

CC InterPro: IPR005467; His_kinase.

CC InterPro: IPR002570; Hpt.

CC InterPro: IPR001789; Response_reg.

CC InterPro: IPR001311; SBP/glu_receptor.

CC InterPro: IPR001638; SBP_bac_3.

CC DR; PF02518; HATPase_c; 1.

CC Pfam; PF00512; HiskA; 1.

CC Pfam; PF00072; response_reg; 1.

CC Pfam; PF00457; SBP_bac_3; 1.

CC PRINTS; PR00344; BCTRLSENSOR.

CC ProDom; PD000039; Response_reg; 1.

CC SMART; SM00387; HATPase_c; 1.

CC SMART; SM00388; HiskA; 1.

CC SMART; SM00073; HPT; 1.

CC SMART; SM00062; PBpb; 2.

CC SMART; SM00448; REC; 1.

CC PROSITE; PS0109; HIS_KIN; 1.

CC PROSITE; PS0894; HPT; 1.

CC PROSITE; PS0110; RESPONSE_REGULATORY; 1.

CC Sensory transduction; Transferase; Kinase; Phosphorylation;

CC Transmembrane; Inner membrane; Signal; Complete proteome.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 1197 SENSOR PROTEIN EVGS.

FT DOMAIN 22 325 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 326 346 POTENTIAL.

FT DOMAIN 347 537 PERIPLASMIC (POTENTIAL).

FT TRANSMEM 538 558 POTENTIAL.

FT DOMAIN 559 1197 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 718 938 HISTIDINE KINASE.

FT DOMAIN 960 1074 RESPONSE REGULATORY.

FT DOMAIN 1098 1197 HPT.

FT MOD_RES 721 721 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 1009 1009 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 1137 1137 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 1197 AA; A01055089D9618E2 CRC64;

Query Match 26.08; Score 176.5; DB 1; Length 1197;

Best Local Similarity 34.48; Pseq No. 4.3e-07;

Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;

OY 12 IKKXNLVLDVDDPLNIIHEIKATIGGISTANNGEEAVIHRDGGSFILMDKEM 71

DB 955 LPEKLSIIADHPTNRLKRLQNLILGVDVDEATDGVQA--LHKVSMQHYDLITVANN 1012

OY 72 PERDGVSTTKKREMEVKSMIVGTVTSLADNEERRAFMEAGLNHCLAKPLTKIKIPLIN 131

DB 1013 PNVDFELTRKLRQNSLPIWGLTANA-QANEREKGLNGMNLCKFKPLTLDVLKTHLS 1071

OY 132 QL 133

DB 1072 QL 1073

RESULT 3

RCSC_SALTI STANDARD; PRT; 948 AA.

AC Q56128;

DT 01-NOV-1997 (Rel. 35, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Sensor protein rscs (EC 2.7.3.-) (Capsular synthesis regulator component C).

GN RCSC OR STY2496 OR T0594.

OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=601;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CT18;

RC MEDLINE=21534947; PubMed=11677608;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;

RA "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";

RL Nature 413:848-852(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Ty2 / ATCC 700931;

RC MEDLINE=22531367; PubMed=12644504;

RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;

RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";

RL J. Bacteriol. 185:2330-2337(2003).

RN [3]

RP SEQUENCE OF 846-948 FROM N.A.

RC STRAIN=Ty2 / ATCC 700931;

RC MEDLINE=96198173; PubMed=8626298;

RA Virlogeux I., Waxin H., Ecobichon C., Lee J.O., Popoff M.Y.;

RA "Characterization of the rcsA and rcsB genes from Salmonella typhi: rcsB through tvIA is involved in regulation of Vi antigen synthesis.";

RL J. Bacteriol. 178:1691-1698(1996).

CC -!- FUNCTION: Member of the two-component regulatory system rscs/rcsB involved in the regulation of the expression of genes involved in colanic acid capsule synthesis. Rscs probably functions as a membrane-associated protein kinase that phosphorylates rcsB in response to environmental signals.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (Probable).

CC -!- PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).

CC -!- SIMILARITY: Contains 1 histidine kinase domain.

CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

CC -!- SIMILARITY: Contains 1 response regulatory domain.

CC

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Qy 78 STTKKUREMEVKSMIVGVTSLADNEERAFNWEAGLNHCLAKPLTKD 124
|:::|::: : |:::| |:::| |:::| |:::| |:::| |:::| |
Db 885 RITRIRPOLGLTLPVVGVTANALAEKRC-LESGMDSCLSPWTL D 930


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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M28242; AAA24503.1; ALT_INIT.
CC EMBL: L11272; AAA24505.1; ALT_INIT.
CC EMBL: AE000311; AAC75278.1; ALT_INIT.
CC EMBL: D90850; BAA16001.1; ALT_FRAME.
CC EMBL: D30850; BAA16006.1; ALT_FRAME.
CC EMBL: D90851; BAA16009.1; ALT_FRAME.
CC EMBL: D90851; BAA16009.1; ALT_FRAME.
CC HSSP: P06143; IUDR.
CC Ecogene: EG10822; rscs.
CC InterPro: IPR003594; ATPbind_ATPase.
CC InterPro: IPR004358; Bact_sens_pr_C.
CC InterPro: IPR003661; His_kinA.
CC InterPro: IPR005467; His_kinase.
CC InterPro: IPR000014; PAS_domain.
CC InterPro: IPR001789; Response_reg.
CC Pfam: PF02518; HATPase_c; 1.
CC Pfam: PF0512; HSKA; 1.
CC Pfam: PF00072; response_reg; 1.
CC PRINTS: PR00344; BCTRLSENSOR.
CC ProDom: PD000039; Response_reg; 1.
CC SMART: SM00387; HATPase_c; 1.
CC SMART: SM00388; HSKA; 1.
CC SMART: SM00091; PAS; 1.
CC SMART: SM00448; REC; 1.
CC PROSITE: PS0109; HIS_KIN; 1.
CC PROSITE: PS0112; PAS; FALSE_NEG.
CC PROSITE: PS0110; RESPONSE_REGULATORY; 1.
CC PROSITE: PS0110; RESPONSE_REGULATORY; 1.
CC Sensor transduction: Transferase; Kinase; Bacterial capsule;
CC Inner membrane; Transmembrane; Phosphorylation; Complete proteome.
CC -----
CC DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 20 41 POTENTIAL.
CC DOMAIN 42 313 PERIPLASMIC (POTENTIAL).
CC TRANSMEM 314 335 POTENTIAL.
CC DOMAIN 336 949 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 357 425 PAS.
CC DOMAIN 476 692 HISTIDINE KINASE.
CC DOMAIN 826 940 RESPONSE REGULATION.
CC MOD_RES 479 479 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC MOD_RES 875 875 PHOSPHORYLATION (BY SIMILARITY).
CC VARIANT 315 315 L -> V (IN STRAIN 09:K30:H12).
CC VARIANT 776 776 K -> E (IN STRAIN 09:K30:H12).
CC VARIANT 890 890 I -> T (IN STRAIN 09:K30:H12).
CC VARIANT 938 938 L -> V (IN STRAIN 09:K30:H12).
CC VARIANT 948 948 D -> E (IN STRAIN 09:K30:H12).
CC CONFLICT 129 130 MR -> IG (IN REF. 1 AND 2).
CC CONFLICT 935 935 T -> S (IN REF. 1).
CC SEQUENCE 949 AA; 106506 MW; E37E9D70EC944A78 CRC64;

Query Match 25.3%; Score 171.5; DB 1; Length 949;
Best Local Similarity 33.9%; Pred. No. 8.6e-07;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 VLIVDDPPLNLIHEKTIKAIGISOTANGGEAVIHRDGGSSFDLIIMDKEMPERGV 77
DB 827 ILVVDDPPIRRLADOLGSLGYCQCTANDGVDAVL--SKNHIDIVLSDYNNPMDGY 884
QY 78 STTKKLEMEVKSIVGVTSIADNEEERRAFRAGNHLCLAKPLTKDKI 126
DB 885 RLTORIQGLTLPVIGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 932

RESULT 6
ID FRZE_MYXXA STANDARD; PRT; 777 AA.
AC P18769;
DT 01-NOV-1990 (Rel. 16, Created)

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01-NOV-1990 (Rel. 16, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Gliding motility regulatory protein (EC 2.7.3.-).
 FRZE
 GN Myxococcus xanthus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 CC Cytophacterales; Myxococcaceae; Myxococcus.
 CX NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90332690; PubMed=2165608;
 RA McCleary W.R., Zusman D.R.;
 RT "Frze of Myxococcus xanthus is homologous to both Chea and Chey of
 RL Salmorella typhimurium".
 RN Proc. Natl. Acad. Sci. U.S.A. 87:5898-5902(1990).
 RP [2]
 PHOSPHORYLATION OF HIS-49.
 RX MEDLINE=91072208; PubMed=2123853;
 RA McCleary W.R., Zusman D.R.;
 RT "Purification and characterization of the Myxococcus xanthus Frze
 RL protein shows that it has autophosphorylation activity".
 RN J. Bacteriol. 172:6661-6668(1990).
 CC -!- FUNCTION: FRZE IS INVOLVED IN A SENSORY TRANSDUCTION PATHWAY THAT
 CC CONTROLS THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING
 CC DIRECTION. FRZE SEEMS TO BE CAPABLE OF AUTOPHOSPHORYLATING ITSELF
 CC ON AN HISTIDINE RESIDUE AND THEN TO TRANSFER THAT GROUP TO AN
 CC ASPARTATE RESIDUE IN THE C-TERMINAL PART OF THE PROTEIN.
 CC -!- SIMILARITY: Contains 1 cheW-like domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 HPT domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: M35192; AAA25396.1; -;
 DR PIR: A35966; A35966.
 DR HSP: Q56310; LB30.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR002545; CheW.
 DR InterPro: IPR003467; His_Kinase.
 DR InterPro: IPR002570; Hpt.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF01584; CheW; 1.
 DR Pfam: PF02518; HATPase_c; 1.
 DR Pfam: PF01627; Hpt; 1.
 DR Pfam: PF00072; Response_reg; 1.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR ProDom: PD000039; Response_reg; 1.
 DR SMART: SM00260; CheW; 1.
 DR SMART: SM00387; HATPase_c; 1.
 DR SMART: SM00073; HPT; 1.
 DR SMART: SM00448; REC; 1.
 DR PROSITE: PS0851; CHEW; 1.
 DR PROSITE: PS50109; HIS_KIN; 1.
 DR PROSITE: PS50894; HPT; 1.
 DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Transference; Kinase; Phosphorylation.
 FT DOMAIN 1 108
 FT DOMAIN 270 509
 FT DOMAIN 511 645
 FT DOMAIN 660 776
 FT MOD_RES 49 49
 FT DOMAIN 130 197
 FT SEQUENCE 777 AA; 83189 MW; 9912BD40991C59E5 CRC64;
 Query Match 23.1%; Score 156.5; DB 1; Length 777;
 Best Local Similarity 35.2%; Pred. No. 1.2e-05;
 Matches 38; Conservative 27; Mismatches 38; Indels 5; Gaps 3;
 Qy 14 KKLNVLYDDPLNLIHKKIIRKIGISQTANGGEAVIIHRDGGSFLLMDKEMPE 73
 Db 657 KRLRVLLVDDSPARATFEGALVGHVVEEADGGEAYV--KVQNTYDILLTDVQMPK 714
 Qy 74 RDGVSTTKKLEMEVKSMI--VGVTSLADNEEERRAFMEAGLNHCLAK 119
 Db 715 LDGFSLARLKLKSTFAVARIPVILLSSLAGSPEDKRRG-LDAGADAYLVK 761
 RESULT 7
 SKN7_YEAST STANDARD; PRT; 622 AA.
 AC P38869; P39747;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 GN Putative transcription factor SKN7 (POS9 protein).
 DE SKN7 OR POS9 OR BRV1 OR YHR206W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94042854; PubMed=8226633;
 RA Brown J.L., North S., Bussey H.;
 RT "SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
 RT beta-glucan assembly, encodes a product with domains homologous to
 RT prokaryotic two-component regulators and to heat shock transcription
 RL J. Bacteriol. 175:6908-6915(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Krens B., Charizanis C., Entian K.-D.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 Du Z., Favell C., Fulton L., Gattling S., Geisel C., Kirsten J.,
 Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
 Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
 Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
 Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RL VIII".
 RL Science 265:2077-2082(1994).
 RN [4]
 RP FUNCTION, AND MUTAGENESIS.
 RX MEDLINE=95045411; PubMed=7957083;
 RA Brown J.L., Bussey H., Stewart R.C.;
 RT "yeast Skn7p functions in a eukaryotic two-component regulatory
 RT pathway".
 RL EMBL J. 13:5186-5194(1994).
 CC -!- FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT
 CC MAY FUNCTION IN A TWO-COMPONENT SIGNAL TRANSDUCTION PATHWAY THAT
 CC ACTS IN PARALLEL WITH THE PKC1 CASCADE TO REGULATE GROWTH AT THE
 CC CELL SURFACE.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
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 CC

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CC -----
DR EMBL: U00485; AAC48911.1; -.
DR EMBL: X83031; CAA58143.1; -.
DR EMBL: U00029; AAB69734.1; -.
DR PIR: A49344; A49344.
DR HSP: P22121; 2HIS.
DR TRANSFAC: T03481; -.
DR SGD: S0001249; SKN7.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0003700; F:transcription factor activity; IDA.
DR GO: GO:000156; F:two-component response regulator activity; IDA.
DR GO: GO:0006350; P:transcription; IDA.
DR InterPro: IPR000232; HSF_DNA_bind.
DR InterPro: IPR002341; HSF_ETS.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF00447; HSF_DNA_bind; 1.
DR Pfam: PF00072; Response_reg; 1.
DR PRINTS: P00056; HSFDOMAIN.
DR ProDom: PD001788; HSF_DNA_bind; 1.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00415; HSF; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE: PS00434; HSF_DOMAIN; 1.
DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
DR Transcription regulation; Sensory transduction: Nuclear protein;
KW DNA-binding; Phosphorylation.
FT DNA_BIND 86 190 BY SIMILARITY.
FT DOMAIN 378 492 RESPONSE_REGULATORY.
FT MOD_RES 427 427 PHOSPHORYLATION (PROBABLE).
FT MUTAGEN 427 427 D->N: DIMINISHED ACTIVITY.
FT MUTAGEN 427 427 D->E: AUGMENTED ACTIVITY.
SQ SEQUENCE 622 AA; 69202 MW; 4C732ED5E326742 CRC64;

Query Match 22.1%; Score 150; DB 1; Length 622;
Best Local Similarity 28.1%; Pred. No. 3.3e-05;
Matches 38; Conservative 32; Mismatches 45; Indels 20; Gaps 4;

QY 12 IRKKNLVIVDDPPLNLIIHEKIIKAIGISQTANNGEAVII---HRDGGSSFDLLIMD 68
-DB 373 LRKGHVLIVDDVDSIGLSKFLRYGCTVQVSDGSLASTLEKRY-----YDLVIMD 427
QY 69 KEMPERDGVSTKKIREMVEKSNIVGVTSADNEERAFNEAGLNHCLAKPLPKDKI-- 126
-DB 428 IYVPLDGTATSIYRSDNEPTPIATMGNIW-QDLITY-QHGNDILAKPFRDRLHS 486.
QY 127 -----IPLINQ 132
-DB 487 ILIRYLKDRIPLCEQ 501

RESULT 8
ARCB_ECO57
ID ARCB_ECO57 STANDARD; PRT; 778 AA.
AC P50363;
DT 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aerobic respiration control sensor protein arcbB (EC 2.7.3.-).
GN ARCB OR 24574 OR ECS4089.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RA MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,

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"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509552;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: Member of the two-component regulatory system arcbB/arcbA.
CC Sensor-regulator protein for anaerobic repression of the arc
CC modulon. Activates arcbA via a four-step phosphorelay. ArcB can
CC also dephosphorylate arcbA by a reverse phosphorelay involving His-
CC 717 and Asp-576 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- PTM: Activation requires a sequential transfer of a phosphate
CC group from a His in the primary transmitter domain, to an Asp in
CC the receiver domain and to a His in the secondary transmitter
CC domain (By similarity).
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC -!- SIMILARITY: Contains 1 HPT domain.
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -!- SIMILARITY: Contains 1 response regulatory domain.
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CC -----
CC EMBL: AF005549; AAG58344.1; -.
CC EMBL: AF002564; BAB37512.1; -.
CC PIR: A91140; A91140.
CC PIR: D85985; D85985.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR002570; Hpt.
DR InterPro: IPR000700; PAS-assoC_C.
DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF00512; HSKA; 1.
DR Pfam: PF00989; PAS; 1.
DR Pfam: PF00072; response_reg; 1.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00387; HATPase_C; 1.
DR SMART: SM00388; HSKA; 1.
DR SMART: SM00073; HPT; 1.
DR SMART: SM00091; PAS; 1.
DR SMART: SM00448; REC; 1.
DR TIGRfams: TIGR00229; sensory_box; 1.
DR PROSITE: PS50109; HIS_KIN; 1.
DR PROSITE: PS50894; HPT; 1.
DR PROSITE: PS50113; PAC; 1.
DR PROSITE: PS50112; PAS; 1.
DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
DR Sensory transduction; Transferase; Kinase; Phosphorylation;
DR Transmembrane; Inner membrane; Transcription regulation;
KW Complete proteome.
KW DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
KW TRANSMEM 26 46 POTENTIAL.
KW DOMAIN 47 57 PERIPLASMIC (POTENTIAL).
KW TRANSMEM 58 78 POTENTIAL.
KW DOMAIN 79 778 CYTOPLASMIC (POTENTIAL).

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EMBL; X53315; CAA37397.1; -
 EMBL; U18997; AAS8012.1; -
 EMBL; A500400; AAC76242.1; -
 EMBL; A501536; AAN44715.1; -
 PIR; D65114; RGEAR.
 PDB; 1A0B; 18-MAR-98.
 PDB; 2A0B; 17-JUN-98.
 PDB; 1BDJ; 11-MAY-99.
 PDB; 1FR0; 31-DEC-02.
 EcoGene; Egl0062; arch.
 InterPro; IPR003594; ATPbind_Atpase.
 InterPro; IPR004358; Bact_sens_pr_C.
 InterPro; IPR003681; His_kinase.
 InterPro; IPR005467; His_kinase.
 InterPro; IPR002570; Hpt.
 InterPro; IPR000700; PAS-associ_C.
 InterPro; IPR000014; PAS_domain.
 InterPro; IPR001789; Response_reg.
 Pfam; PF02518; HATPase_c; 1.
 Pfam; PF00512; HSKA; 1.
 Pfam; PF00989; PAS; 1.
 Pfam; PF00072; response_reg; 1.
 PRINTS; PR00344; BCTRLSENSOR.
 ProDom; PD000039; Response_reg; 1.
 SMART; SM00388; HSKA; 1.
 SMART; SM00073; HPT; 1.
 SMART; SM00091; PAS; 1.
 SMART; SM00448; REC; 1.
 TIGRfams; TIGR00229; sensory_box; 1.
 PROSITE; PS0109; HIS_KIN; 1.
 PROSITE; PS00894; HPT; 1.
 PROSITE; PS0113; PAC; 1.
 PROSITE; PS0112; PAS; 1.
 PROSITE; PS0110; RESPONSE_REGULATORY; 1.
 Sensory transduction; Transferrase; Kinase; Phosphorylation;
 Transmembrane; Inner membrane; Transcription regulation; 3D-structure;
 Complete proteome.
 FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 26 46 POTENTIAL.
 FT DOMAIN 47 57 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 POTENTIAL.
 FT DOMAIN 79 778 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 153 223 PAS.
 FT DOMAIN 226 278 PAC.
 FT DOMAIN 289 507 HISTIDINE KINASE.
 FT DOMAIN 527 643 RESPONSE REGULATORY.
 FT DOMAIN 678 771 HPT.
 FT MOD_RES 292 292 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 576 576 PHOSPHORYLATION (PROBABLE).
 FT MOD_RES 717 717 PHOSPHORYLATION (PROBABLE).
 FT MUTAGEN 292 292 H->Q: LOSS OF ACTIVITY.
 FT MUTAGEN 576 576 D->A: LOSS OF ACTIVITY.
 FT MUTAGEN 717 717 H->Q: LOSS OF ACTIVITY.
 FT CONFLICT 469 470 MISSING (IN REF. 2).
 SEQUENCE 778 AA; 87982 MW; DD61EA6ECF95AD30 CRC64;
 Query Match 22.18; Score 149.5; DB 1; Length 778;
 Best Local Similarity 25.64; Pred. No. 4.6e-05;
 Matches 31; Conservative 40; Mismatches 47; Indels 3; Gaps 2;
 QY 16 LNVLIVDDPLNLIIHEKIIKAIGISQTANNGEAVIIHRDGGSGFDLILDKEMPERD 75
 Db 526 LNVLLVEDIENVIVARSVLEKLSNVDVAMTKAALMEKPG-EYDLVLLDIQLPDMT 583
 QY 76 GVSTTKKUREMEVSMGVTVSLADNE-EERRAFMEAGLNHCLAKPLTKDKIPLNQLM 134
 Db 584 GLDISRELTQKYPREDLPPLVALTANVLYKQKQEVNAGMDVLSKPLSPALITAMIKFEW 643
 QY 135 D 135
 Db 644 D 644

RESULT 10
 SLN1_YEAST STANDARD; PRT; 1220 AA.
 ID SLN1_YEAST
 AC P39928;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Osmolarity two-component system protein SLN1 (EC 2.7.3.-).
 GN SLN1 OR YPD2 OR YII147C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / YPH1;
 RX MEDLINE=94024010; PubMed=8211183;
 RT Ota I.M., Varshavsky A.;
 RT "A yeast protein similar to bacterial two-component regulators.";
 RL Science 262:566-569(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RX PubMed=9169870;
 RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
 RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
 RA Moulis S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
 RA Skelton J., Smith V., Walsh S., Whitehead S., Barrett B.G.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
 RL Nature 387:84-87(1997).
 RN [3]
 RP MUTAGENESIS OF HIS-576 AND ASP-1144.
 RX MEDLINE=94239498; PubMed=8183345;
 RA Maeda T., Wurgler-Murphy S.M., Saito H.;
 RT "A two-component system that regulates an osmosensing MAP kinase
 cascade in yeast.";
 RL Nature 369:242-245(1994).
 CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
 SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
 EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK22->
 PBS2->HOG1 PATHWAY. INACTIVE SLN1 ALLOWS THE UNPHOSPHORYLATED SSK1
 PROTEIN TO ACTIVATE SSK2 AND SSK22, TWO MAPKKS THAT FURTHER
 STIMULATE THE PBS2-HOG1 MAPK CASCADE. IN LOW OSMOLARITY MEDIA,
 THE ACTIVATED SLN1 HISTIDINE KINASE REPRESSSES THE ACTIVATION OF THE
 PBS2-HOG1 KINASE CASCADE THROUGH PHOSPHORYLATION OF SSK1.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
 BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND AN ASP OF THE RECEIVER
 DOMAIN.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
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 CC EMBL; Z38059; CAA86131.1; -
 CC EMBL; U01835; AAC48912.1; -
 CC PIR; S48387; S48387.
 CC HSSP; P06143; 1UDR.
 CC SGD; S0001409; SLN1.
 CC GO; GO:0007234; P:osmosensory signaling pathway via two-compo. . . ; IDA.
 CC GO; GO:0042542; P:response to hydrogen peroxide; IMP.
 CC InterPro; IPR003594; ATPbind_Atpase.
 CC InterPro; IPR004358; Bact_sens_pr_C.
 CC InterPro; IPR003681; His_kinase.
 CC InterPro; IPR005467; His_kinase.
 CC InterPro; IPR001789; Response_reg.

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sensor protein gacS (EC 2.7.3.-).
 GN GACS OR LEMA.
 OS Pseudomonas syringae (pv. syringae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=321;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92234961; PubMed=1314807;
 RA Hrabak E.M., Willis D.K.;
 RT "The lema gene required for pathogenicity of Pseudomonas syringae pv.
 syringae on bean is a member of a family of two-component
 regulators."
 RL J. Bacteriol. 174:3011-3020(1992).
 CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
 GACA/GACS(LEMA). MAY BE INVOLVED IN LESION FORMATION, SWARMING AND
 IN THE PRODUCTION OF EXTRACELLULAR PROTEASE, SYRINGOMYCIN AND N-
 ACYL-L-HOMOSERINE LACTONE (ACYL-HSL). REQUIRED FOR PATHOGENICITY
 ON BEAN.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 (Probable).
 CC -!- PTM: Activation requires a sequential transfer of a phosphate
 group from a His in the primary transmitter domain, to an Asp in
 the receiver domain and to a His in the secondary transmitter
 domain (By similarity).
 CC -!- SIMILARITY: Contains 1 HAMP domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 HPT domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC
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 CC
 CC EMBL; M80477; AAA25877.1; --
 DR HSPP; P06143; IUDR.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR003660; HAMP.
 DR InterPro: IPR003661; His_kinA.
 DR InterPro: IPR005467; His_kinase.
 DR InterPro: IPR002570; Hpt.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00672; HAMP; 1.
 DR Pfam: PF02518; HATPase_C; 1.
 DR Pfam: PF00512; Hiska; 1.
 DR Pfam: PF01627; Hpt; 1.
 DR Pfam: PF00072; Response_reg; 1.
 DR PRINTS; PR00344; BCTRLENSOR.
 DR PRODOM; PDD000039; Response_reg; 1.
 DR SMART; SM00304; HAMP; 1.
 DR SMART; SM00387; HATPase_C; 1.
 DR SMART; SM00388; Hiska; 1.
 DR SMART; SM00073; HPT; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50885; HAMP; 1.
 DR PROSITE; PS50109; HIS_KIN; 1.
 DR PROSITE; PS50894; HPT; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Transpherase; Kinase; Phosphorylation;
 KW Transmembrane; Inner membrane.
 FT TRANSMEM 9 25 POTENTIAL.
 FT TRANSMEM 84 101 POTENTIAL.
 FT TRANSMEM 159 178 POTENTIAL.
 FT DOMAIN 182 234 HAMP.
 FT DOMAIN 281 502 HISTIDINE KINASE.
 FT DOMAIN 658 777 RESPONSE REGULATORY.
 FT DOMAIN 814 907 HPT.

FT MOD_RES 284 284 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 707 707 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 853 853 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 907 AA; 99195 MW; 5B9F4663DAF3492C CRC64;
 Query Match 20.98; Score 142; DB 1; Length 907;
 Best Local Similarity 27.68; Pred. No. 0.00023;
 Matches 35; Conservative 33; Mismatches 33; Indels 26; Gaps 4;
 QY 18 VLIVDDPLNLTIIHKIKKIGGISTQANNNGEAVIHRDGG-----SFDILMD 68
 DB 659 VLVVDNPNANLLVQTLLEDNG-----AEVVAEGGYAAVNAVQAEFDVLMD 707
 QY 69 KEMPERDGVSTTKKLENEVKS-----MIVGVTSIADNEERERAFMEAGNHCLAKPLTK 123
 DB 708 VQPMGDGRQATEAIRAWEARNOSLPIVALTAHA-MANEKRSLLQSGMDYLTKEPSE 766
 QY 124 DKRIIPLI 130
 DB 767 RQLAQVW 773
 RESULT 13
 DCTR_BACSU STANDARD; PRT; 226 AA.
 ID DCTR_BACSU AC P56602; P94503;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable C4-dicarboxylate response regulator dctr.
 GN DCTR.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
 RT "A 148 kbp sequence of the region between 35 and 47 degree of the
 Bacillus subtilis genome."
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Borriess R., Boursier L., Brans A., Braun M., Brignall S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Maestri D., Nakai S., Noback M.,
 Medina N., Mellado R.P., Mizuno M., Moesti D., Oudega B., Park S.H.,
 Noore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Prascan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Solido B.,
 Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 Viari A., Wambutt R., Wedler E., Wedler K., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

"The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*,"
 Nature 390:249-256(1997).
 [3]
 SEQUENCE OF 14-101 FROM N.A.
 STRAIN=SB202; PubMed=9168601;
 MEDLINE=97311990; PubMed=9168601;
 Morel-Deville F., Ehrlich S.D., Morel P.;
 "Identification by PCR of genes encoding multiple response
 regulators,"
 Microbiology 143:1513-1520(1997).
 [4]
 FUNCTION, AND GENE NAME.
 RT STRAIN=168; PubMed=10708364;
 RX MEDLINE=20170658; PubMed=10708364;
 RA Asai K., Baik S.-H., Kasahara Y., Moriya S., Ogasawara N.;
 "Regulation of the transport system for C4-dicarboxylic acids in
Bacillus subtilis,"
 Microbiology 146:263-271(2000).
 RL Microbiology 146:263-271(2000).
 CC -!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
 CC -!- ESSENTIAL FOR EXPRESSION OF DCTP.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- PTM: PHOSPHORYLATED BY DCTS (PROBABLE).
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB001488; BAA19283.1; -
 DR EMBL; 299106; CAB12253.1; -
 DR EMBL; 082880; AAB41751.1; -
 DR PIR; B69771; B69771.
 DR HSP; Q56312; ITWY.
 DR Subtilist; BG12074; dctr.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF00072; response_reg; 1.
 DR PIRSF; PIRSF006171; RR_citrat_malat; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00448; REC; 1.
 DR HSP; Q56312; ITWY.
 DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
 DR Sensory transduction; Transcription regulation; DNA-binding;
 KW Activator; Phosphorylation; Complete proteome.
 FT DOMAIN 7 123 RESPONSE REGULATORY.
 FT MOD_RES 58 58 PHOSPHORYLATION (BY SIMILARITY).
 FT DNA_BIND 176 206 H-T-H MOTIF (POTENTIAL).
 FT CONFLICT 24 24 F -> I (IN REF. 3).
 SQ SEQUENCE 226 AA; 25539 MW; 018115B14E9EF47D CRC64;
 Query Match 20.7%; Score 140.5; DB 1; Length 226;
 Best Local Similarity 25.9%; Pred. No. 6.7e-05;
 Matches 30; Conservative 39; Mismatches 42; Indels 5; Gaps 3;
 QY 13 KKLNVLIIVDDPLNLIHEKIIKAIGIS--QTANNNGEAAVHHRDGSGSFLLMDKE 70
 Db 3 RREKVLIEDDPVQVQVNVKFFITVKGTVTCATAGNGEEMGLIKE--EQPDVLVDVY 60
 QY 71 MPEDGVSTTKKLEMEVKSIVGTSLADNEERAFRAEAGLNHCLAKPLTKDKI 126
 Db 61 MPKKGDIKTLQIRKQKLEVDVI-VVSAKDKETISLMLQNGAYDYLKPKFLERM 115
 RESULT 14
 DCTR_BACHD STANDARD; PRT: 230 AA.
 AC Q9K998;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Probable C4-dicarboxylate response regulator dctr.
 GN DCTR OR BH2751.
 OS *Bacillus halodurans*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=86665;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 Horikoshi K.;
 "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
halodurans and genomic sequence comparison with *Bacillus subtilis*,"
 Nucleic Acids Res. 28:4317-4331(2000).
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
 CC -!- ESSENTIAL FOR EXPRESSION OF DCTP (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- PTM: PHOSPHORYLATED BY DCTS (BY SIMILARITY).
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AP001516; BAB06470.1; -
 DR PIR; G83993; G83993.
 DR HSP; P10957; LRNL.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF00072; response_reg; 1.
 DR PIRSF; PIRSF006171; RR_citrat_malat; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
 DR Sensory transduction; Transcription regulation; DNA-binding;
 KW Activator; Phosphorylation; Complete proteome.
 FT DOMAIN 8 124 RESPONSE REGULATORY.
 FT MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
 FT DNA_BIND 183 209 H-T-H MOTIF (POTENTIAL).
 FT CONFLICT 230 AA; 26376 MW; 06FD65F46FC57D40 CRC64;
 SQ SEQUENCE 230 AA; 26376 MW; 06FD65F46FC57D40 CRC64;
 Query Match 20.7%; Score 140.5; DB 1; Length 230;
 Best Local Similarity 29.4%; Pred. No. 6.9e-05;
 Matches 35; Conservative 32; Mismatches 47; Indels 5; Gaps 3;
 QY 16 LNLIVDDPLNLIHEKIIKAIG--ISQTANNNGEAAVHHRDGSGSFLLMDKEMPE 73
 Db 7 IRLVIEDDPVQVQVNVKFFITVKGTVTCATAGNGEEMGLIKE--EQPDVLVDVY 64
 QY 74 RGVSTTKKLEMEVKSIVGTSLADNEERAFRAEAGLNHCLAKPLTKDKIPLNQ 132
 Db 65 QDGLSFIKQIREQIDVDIIAVTA-ANDTKITLLRYGVMDYLVKPFTEERLKAALQ 122
 RESULT 15
 CHEV_BACSU STANDARD; PRT: 119 AA.
 ID CHEV_BACSU
 AC P24072; P37583;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chemotaxis protein chev homolog.
 GN CHEV OR CHEB.
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=1423;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=168 / 011085;

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M59781; AAA22311.1; -
DR EMBL; 299112; CAB13506.1; -
DR EMBL; M86738; AAA22450.1; -
DR EMBL; M87005; AAA22451.1; -
DR PIR; A40874; A40874.
DR HSSP; Q56312; ITMY.
DR Subtilisin; BG10258; chev.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Chemotaxis; Sensory transduction; Phosphorylation; Complete proteome.
FT INIT_MET 0 0
FT DOMAIN 1 118 RESPONSE_REGULATORY.
FT MCD_RES 53 53 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 119 AA; 13178 MW; F3BCA0F02CAB7531 CRC64;

Query Match 19.8%; Score 134; DB 1; Length 119;
Best Local Similarity 26.9%; Pred. No. 0.00012;
Matches 32; Conservative 36; Mismatches 47; Indels 4; Gaps 3;

QY 18 VLIVDDDP-LNLIIEKIKAIGGISQTANNGEAEVVIHRDGGSSFDLIIMDKEMPERDG 76
Db 4 ILIVDDAFAFMWIKDILVKNGFVVAEAGQAQAVEYKE--HSPDLVTWDTIMPMDG 61
QY 77 VSTTKKLEMEVKSMIVGVTSVLADNEERERRPMEAGLNHCLAKPLTKDKIIPNLQMD 135
Db 62 ITALKEIKQIDAQARIIMCSAMGQOSMVIDA-IOAGAKDFIVKFPQADRVLEAIKNTLN 119

Search completed: August 14, 2003, 16:47:19
Job time : 24 secs

RX MEDLINE=91286247; PubMed=1905718;
RA Bischoff D.S., Ordal G.W.;
RT "Sequence and characterization of Bacillus subtilis Chep, a homolog
of Escherichia coli CheY, and its role in a different mechanism of
RT Chemotaxis";
RL J. Biol. Chem. 266:12301-12305(1991).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borliss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devigne K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetle D., Porwollik S., Prescott A.M.,
RA Prascan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpsira P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vanier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis";
RL Nature 390:249-256(1997).
RN [3]
RN SEQUENCE OF 1-7 FROM N.A.
RC STRAIN=168 / OI1085;
RC MEDLINE=93078625; PubMed=1447979;
RX Bischoff D.S., Ordal G.W.;
RT "Identification and characterization of fliY, a novel component of
the Bacillus subtilis flagellar switch complex";
RL Mol. Microbiol. 6:2715-2723(1992).
RN [4]
RN SEQUENCE OF 95-119 FROM N.A.
RC STRAIN=168 / OI1085;
RC MEDLINE=92283757; PubMed=1597417;
RX Bischoff D.S., Weinreich M.D., Ordal G.W.;
RT "Nucleotide sequences of Bacillus subtilis flagellar biosynthetic
genes fliP and fliQ and identification of a novel flagellar gene,
fliZ";
RL J. Bacteriol. 174:4017-4025(1992).
RN [5]
RN SEQUENCE OF 1-12.
RC STRAIN=168 / JH642;
RC MEDLINE=96345629; PubMed=8755892;
RX Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis";
RL J. Bacteriol. 178:4611-4619(1996).
CC -1- FUNCTION: HAS A CENTRAL CONTROLLING ROLE IN CHEMOTAXIS. ALTHOUGH
IT IS HOMOLOGOUS TO THE CHEY PROTEIN OF OTHER BACTERIA, IT IS
THOUGHT TO FUNCTION IN A DIFFERENT MANNER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Contains 1 response regulatory domain.
CC -----
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OM protein - protein search, using sw model

Run on: August 14, 2003, 16:46:47 ; Search time 95 Seconds

(without alignments)
369.423 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MATKSMGDIEKIKKLNVL.....LAKPLTKDKIPLINQLMDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp-archaea:*

2: sp-bacteria:*

3: sp-fungi:*

4: sp-human:*

5: sp-invertebrate:*

6: sp-mammal:*

7: sp-misc:*

8: sp-organelle:*

9: sp-phage:*

10: sp-plant:*

11: sp-rodent:*

12: sp-virus:*

13: sp-vertebrate:*

14: sp-unclassified:*

15: sp-virus:*

16: sp_bacteriap:*

17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	136	10	O82445
2	538	79.4	142	10	Q9M8Y4
3	181	26.7	1969	5	O15763
4	179.5	26.5	820	16	Q8E263
5	178.5	26.3	1197	16	Q8CVU5
6	174	25.7	394	16	Q9A3P0
7	173.5	25.6	949	16	Q8FFP9
8	173	25.5	417	2	Q9RLC7
9	171.5	25.3	933	16	Q8XE39
10	171.5	25.3	957	16	Q8ZGR4
11	171	25.2	927	2	Q9ANY0
12	170	25.1	769	16	Q8PQ37
13	167.5	24.7	1364	16	Q8PUN8
14	166.5	24.6	507	2	Q8S663
15	163.5	24.1	1364	16	Q8F883
16	162.5	24.0	642	16	Q9A3L2

17 162.5 24.0 719 3 Q9P896
18 162.5 24.0 778 16 Q8ZB69
19 162 23.9 767 16 Q8PD62
20 161.5 23.8 148 5 Q9GTU0
21 161.5 23.8 1709 5 Q9SPH5
22 161 23.7 716 16 Q8D5I6
23 160.5 23.7 574 16 Q8D9H9
24 159.5 23.5 571 16 Q8O4E1
25 159 23.5 117 17 Q28381
26 159 23.5 736 16 Q9KR16
27 159 23.5 1645 16 Q8YVW3
28 158.5 23.4 1266 3 Q8NIV2
29 157 23.2 900 16 Q9AC40
30 156.5 23.1 469 2 Q8RNK0
31 156 23.0 1000 17 Q8TPA1
32 155 22.9 690 16 Q9A501
33 155 22.9 767 12 Q8QV7
34 154.5 22.8 122 17 Q28867
35 154.5 22.8 572 16 Q9KSI6
36 154 22.7 708 3 Q9C1Q7
37 154 22.7 848 2 Q9AEW3
38 153.5 22.6 713 16 Q9A472
39 153.5 22.6 939 2 Q8KWS5
40 153 22.6 1268 2 Q8KQV0
41 152.5 22.5 120 17 Q48299
42 152.5 22.5 514 16 Q9ABT2
43 152.5 22.5 929 16 Q8EBQ2
44 152.5 22.5 935 2 Q8RMF4
45 152.5 22.5 1068 16 Q8PM23

ALIGNMENTS

RESULT 1

O82445 PRELIMINARY: PRT: 136 AA.
ID O82445
AC O82445;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Response regulator protein.
DE Response regulator protein.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitelaw C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;
RT "A mRNA encoding a response regulator protein from Brassica napus is up-regulated during pod development.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF057027; AAC62225.1;
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg.1.
DR ProDom; PD000039; Response_reg.1.
DR SMART; SM00448; REC.1.
DR PROSITE; PS01110; RESPONSE_REGULATORY.1.
KW Phosphorylation; Sensory transduction.
SQ SEQUENCE 136 AA; 15035 MW; DA99B768FAB3CFP5 CRC64;

Query Match 100.0%; Score 678; DB 10; Length 136;
Best Local Similarity 100.0%; Pred. No. 4,7e-52;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATKSMGDIEKIKKLNVLIVDDOPLNLIIEKIIKAIIGGISQTANNNGEAVIIHRDGS 60
Db 1 MATKSMGDIEKIKKLNVLIVDDOPLNLIIEKIIKAIIGGISQTANNNGEAVIIHRDGS 60
Qy 61 SFDLILMDKEMPERGVSTTKKREMEYKSMIVGVTSIADNEEERRAFMEAGLNHCLAKP 120
Db 61 SFDLILMDKEMPERGVSTTKKREMEYKSMIVGVTSIADNEEERRAFMEAGLNHCLAKP 120

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QY 121 LTKDKIPLINQMDA 136
DB 121 LTKDKIPLINQMDA 136
RESULT 2
Q9M8Y4 PRELIMINARY; PRT; 142 AA.
AC Q9M8Y4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative response regulator protein (receiver component).
GN T6K12.10.
OS Arabidopsis thaliana (Mouse-ear cress);
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Rongning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T6K12 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Trouthan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.B.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Braver V., Trouthan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC016829; AAF26786.1; -
DR EMBL; AY085638; AAM62859.1; -
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; response_reg.1.
DR ProDom; PD000039; Response_reg.1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Phosphorylation; Sensory transduction.
KW Phosphorylation, Sensory transduction.
SQ SEQUENCE 142 AA; 15792 MW; 57487135FF2D5238 CRC64;

Query Match 79.4%; Score 538; DB 10; Length 142;
Best Local Similarity 78.9%; Pred. No. 9.8e-40;
Matches 112; Conservative 8; Mismatches 16; Indels 6; Gaps 2;

QY 1 MATKSMGDIK-----IKKKL-NLVIVDDPLNLIHEKIIKAIIGISQTANNGEAAVII 54
DB 1 MATKSTGTETKSIKLVKKLNVLIVDDPLNRLRHEMIKTIIGISQTAKNGEAAVII 60
QY 55 HRDGGSFILMDKMPERDGVSTTKKLRMEVKSMIVGVTSIADNEERAFMEAGLN 114
DB 61 HRDGEASFILMDKMPERDGVSTTKKLRMKVTSIADNEERAFMEAGLN 120
QY 115 HCLAKPLTKKIPLINQMDA 136
DB 121 HCLAKPLTKKIPLINQMDA 142
RESULT 3
O15763 PRELIMINARY; PRT; 1969 AA.
AC O15763;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

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DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hybrid histidine kinase DHKB.
GN DHKB.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KAX3;
RX MEDLINE=98248997; PubMed=9576830;
RA Zinda M.J., Singleton C.K.;
RT "The hybrid histidine kinase dhkb regulates spore germination in
RT Dictyostelium discoideum.";
RL Dev. Biol. 196:171-183(1998).
DR EMBL; AF024654; AAB71889.1; -
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_KinA.
DR InterPro; IPR003467; His_Kinase.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HarPase_C; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg.1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg.1.
DR SMART; SM00387; HarPase_C; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR TIGRfams; TIGR00229; sensory_box; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1969 AA; 219025 MW; 857A7952AB1B528 CRC64;

Query Match 26.7%; Score 181; DB 5; Length 1969;
Best Local Similarity 35.8%; Pred. No. 5.1e-07;
Matches 48; Conservative 29; Mismatches 39; Indels 18; Gaps 5;

QY 10 EKIKKKLVIVDDPLNLIHEKIIKAIIGISQTANNGEAAVIIHRDGGSFILMDK 69
DB 1836 EKIEK---ILVEDNFYVNFVIFSKLLKDSGYIFDVAHNGVEAVECYKKG--AYDILMD 1890
QY 70 EMERDGVSTTKKLRMEVKSMI-----VGVTSLADNE--EERRAFMEAGLNHCL 117
DB 1891 QMPENDGFEATTAIRELEKSNLIESPPSKKSHVIVALTANSYKDKGKCLSGVGMNDFL 1950
QY 118 AKPL-TDKKIPLI 130
DB 1951 OKPIKTSIDILQMI 1964
RESULT 4
Q8EZ63 PRELIMINARY; PRT; 820 AA.
AC Q8EZ63;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Two-component hybrid sensor and regulator.
GN LA3996.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011554; AAN51193.1; -
KW Complete proteome.
SQ SEQUENCE 820 AA; 94325 MW; 3DBE99966794E67D CRC64;

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Query Match          26.5%; Score 179.5; DB 16; Length 820;
Best Local Similarity 31.6%; Pred. No. 2.4e-07;
Matches 43; Conservative 29; Mismatches 49; Indels 15; Gaps 5;

QY      8 DIEK-----IKKLNVLIVDDPLNLIIEKIIKAIGGISQTANNGEAVIIHRDGGSSF 62
DB      679 DLEKSFQDVVAKSTRILVAEDNETNCLLIERALKKLGVDPTVVHNGRE--VIERMQLEAF 736

QY      63 DLILMDKEMPERGVSTTKKIREMEVKS---MIVGVTSIADNEEBERAFMEAGLNHCLAK 119
DB      737 DIILMDHMPEDVIGIEATKWRKSNSEFFIIIALTADA-ISSKERYIKSGMMDCLTK 795

QY      120 PLTKDKRIPLINLMD 135
DB      796 PLD-----LPIKSTLD 807

RESULT 5
Q8CVU5 PRELIMINARY; PRT; 1197 AA.
AC Q8CVU5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE Sensor protein evgs precursor (EC 2.7.3.-).
GN EVGS OR C2906.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.J., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016764; AA81356.1; -.
KW Transferase; Complete proteome.
SQ SEQUENCE 1197 AA; 134847 MW; 5088214E7F834F06 CRC64;

Query Match          26.38; Score 178.5; DB 16; Length 1197;
Best Local Similarity 34.4%; Pred. No. 4.6e-07;
Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;

QY      12 IKKLNVLIVDDPLNLIIEKIIKAIGGISQTANNGEAVIIHRDGGSSFDLILMDKEM 71
DB      955 LPKXLSILIADHDPTNRLKQLNLLGVDVDEATDGVQA--LHKYSMQHYDLITDVNM 1012

QY      72 PERGVSTTKKIREMEVKSIVGVTSIADNEEBERAFMEAGLNHCLAKPLTKDKIPLIN 131
DB      1013 FNMDFELTRKLRQNSLSPIWGLTANA-QANEREXGLNGMNLCLFKPLTLDVLKTHLS 1071

QY      132 QL 133
DB      1072 QL 1073

RESULT 6
Q9A3P0 PRELIMINARY; PRT; 394 AA.
AC Q9A3P0;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE Sensor histidine kinase/response regulator.
GN CC3162.
OS Caulobacter crescentus.
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OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OX Caulobacteraceae; Caulobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nielsen W.C., Felblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit K., Craven M.B., Khouri H., Shetty J., Barry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
DR EMBL; AE005980; AAK25124.1; -.
DR HSP; Q06657; 2CHF.
DR TIGR; CC3162; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR005467; His_Kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c.1.
DR Pfam; PF00072; response_reg.1.
DR ProDom; PD000039; Response_reg.1.
DR SMART; SM00387; HATPase_c.1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01019; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction; Complete proteome.
SQ SEQUENCE 394 AA; 41592 MW; 6D9AF0B278B70E70 CRC64;

Query Match          25.7%; Score 174; DB 16; Length 394;
Best Local Similarity 31.7%; Pred. No. 3.1e-07;
Matches 39; Conservative 31; Mismatches 49; Indels 4; Gaps 2;

QY      14 KKNLVIVDDPLNLIIEKIIKAIGGISQTANNGEAVIIHRDGGSSFDLILMDKEMPE 73
DB      262 RSAHLIVDDNATNRVVAEALCDMFECTSEQAVDGVAEVEMARSG--REDLILMDIKMP 319

QY      74 RDGVSTTKKIREMEVKSIVGVTSIADNEE--ERRAFMEAGLNHCLAKPLTKDKIPLIN 131
DB      320 MDGVAATRAIRELSGRSSAAPIVALTANADPADVHTYLAAGMDQVVVEKPIKPERLALVN 379

QY      132 QLM 134
DB      380 SLL 382

RESULT 7
Q8FFP9 PRELIMINARY; PRT; 949 AA.
AC Q8FFP9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE Sensor protein rcsc (EC 2.7.3.-).
GN RCSC OR C2761.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX Enterobacteriaceae; Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.J., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
```

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RT of uropathogenic Escherichia coli.;
RL PROC. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016763; AAN81215.1; -.
SQ Transferrase; Complete proteome.
KW SEQUENCE 949 AA; 106590 MW; DF8CA47F9EEB4088 CRC64;

Query Match      25.6%; Score 173.5; DB 16; Length 949;
Best Local Similarity 33.6%; Pred. No. 9.7e-07;
Matches 37; Conservative 35; Mismatches 37; Indels 5; Gaps 3;

QY 18 VLIYDDDPNLIIHEKIIKAIGGISQTANGGEAV-IHRDGGSSFDLLIMDKEMPERDG 76
Db :|||:||: : : |||:||: : : : : |||:||: : : |||
827 ILVVDOPHINRRLDAGSLGSGCTEANDGVDAIYNLNK---NHIDIVLSVDNPNMMDG 883
QY 77 VSTTKKLREMEVKSVMIGVTSLADNEEFERAFRAEAGLNHCLAKPLTKDKI 126
Db :|||:||: : : |||:||: : : |||:||: : : |||
884 YELQRIQRILGLTLPVIGVTANALAEKQRC-LESGMDSCLSPVTLDVI 932

RESULT 8
Q9RLC7 PRELIMINARY; PRT; 417 AA.
AC Q9RLC7;
DT 01-MAY-2000 (TrEMBLrel. 13), Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative histidine kinase (Fragment).
GN GACS.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JW300;
RA Grapner S.; Wackernagel W.; EMBL/GenBank/DBJ databases.
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249741; CAB56474.1; -.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00073; HPT; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR KW Kinase; Phosphorylation; Sensory transduction.
FT NON_TER 1
SQ SEQUENCE 417 AA; 45749 MW; D196B4FFDDA23BE2 CRC64;

Query Match      25.5%; Score 173; DB 2; Length 417;
Best Local Similarity 32.8%; Pred. No. 4e-07;
Matches 39; Conservative 35; Mismatches 37; Indels 8; Gaps 3;

QY 17 NVLIYDDDPNLIIHEKIIKAIGGISQTANGGEAV-IHRDGGSSFDLLIMDKEMPERDG 76
Db :|||:|||: : : : : |||:||: : : |||:||: : : |||
169 SVLYCDNDPANMLLETLTDMGGEVAVSQQALEVQQ--QSFDWMFMVQMFGMDG 226
QY 77 VSTTKKLREMEVKS-----MIVGVTSLADNEEFERAFRAEAGLNHCLAKPLTKDKIPLI 130
Db :|||:||: : : |||:||: : : |||:||: : : |||:||: : : |||
227 RQTEAIRWELESQPPIPALVATAHA-LSNERRSLQLSGDLTLTKPKISERQLAQVV 284

RESULT 9
Q8XE39 PRELIMINARY; PRT; 933 AA.
AC Q8XE39;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sensor for ctr capsule biosynthesis, probable histidine kinase
DE acting on RcsB.
OS RCSC OR Z3477 OR ECS107.
GN Escherichia coli O157:H7.
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RX MEDLINE=21142508; PubMed=11208780;
RA Visick K.L., Skoufos L.M.
RT "A two-component sensor required for normal symbiotic colonization of
RL Euprymna scolopes by Vibrio fischeri."
RL J. Bacteriol. 183:835-842(2001).
CC -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
DR EMBL: AF319618; AAG60694.1; -.
DR InterPro: IPR003594; AtPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR003467; His_kinase.
DR InterPro: IPR002570; Hpt.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-assoc_C.
DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF02518; HATPase_C; 1.
DR Pfam: PF06512; HiskA; 1.
DR Pfam: PF01627; HPT; 1.
DR Pfam: PF00785; PAC; 1.
DR Pfam: PF00989; PAS; 1.
DR Pfam: PF00072; response_reg; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00387; HATPase_C; 1.
DR SMART: SM00388; HiskA; 1.
DR SMART: SM00073; HPT; 1.
DR SMART: SM00086; PAC; 1.
DR SMART: SM00091; PAS; 1.
DR SMART: SM00448; REC; 1.
DR TIGRfams: TIGR00229; sensory_box; 1.
DR PROSITE: PS50109; HIS_KIN; 1.
DR PROSITE: PS50113; PAC; 1.
DR PROSITE: PS50112; PAS; 1.
DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
DR KINASE: Phosphorylation; Sensory transduction; Transferase.
KW KINASE
SQ SEQUENCE 927 AA; 105590 MW; 9EE0659CB2E8BF8B CRC64;

Query Match 25.2%; Score 171; DB 2; Length 927;
Best Local similarity 33.9%; Pred. No. 1.6e-06;
Matches 43; Conservative 28; Mismatches 42; Indels 14; Gaps 4

QY 16 LNVLIIVDDPLNLIHEKIIKRAIGISQTANNNGEAVIIHRDGGSGFDLILMDKEMPERD 75
DB 659 LSIIIAEDKNALVAQMFQRLGHKATIAENGK--VAIDKLKETHFDLIINDNHPVMD 716
QY 76 GYSTTKKRE-MEVKSMIVGVTSLA-----DNESERRAFMEAGINHCLAKPLTKDKIPL 129
DB 717 GLIATKIIREKLKISTVIFAYTANAFKAHDN-----FLKAGANYVITXPLQENDFIGA 770
QY 130 INQLMDA 136
DB 771 IKYQDA 777

RESULT 12
Q8PQ37 PRELIMINARY; PRT: 769 AA.
ID Q8PQ37
AC Q8PQ37;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component system sensor protein.
DE GN XAC0494.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;

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RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furian L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Canavan F., Cardozo J., Chamberg F., Ciapina L.P.,
 RA Cicarilli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado N.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Weidman J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spínola L.A.F., Takita M.A., Tamara R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities";
 RL Nature 417:459-463(2002).
 DR EMBL: AE011676; AM35383.1; -
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR003661; His_kinA.
 DR InterPro: IPR005467; His_kinase.
 DR InterPro: IPR002570; Hpt.
 DR Pfam: PF02518; HATPase_C.1.
 DR Pfam: PF00512; HiskA.1.
 DR Pfam: PF01627; Hpt.1.
 DR Pfam: PF00989; PAS.2.
 DR Pfam: PF00072; response_reg.2.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR PRODOM: PD000039; Response_reg.1.
 DR PROSITE: PS0109; HIS_KIN.1.
 DR PROSITE: PS0110; RESPONSE_REGULATORY.1.
 KW Complete proteome.
 SQ SEQUENCE 769 AA; 83699 MW; B7995CA40A787593 CRC64;

Query Match 25.1%; Score 170; DB 16; Length 769;
 Best Local Similarity 30.5%; Pred. No. 1.5e-06;
 Matches 36; Conservative 38; Mismatches 36; Indels 8; Gaps 3;

QY 14 KLNVLIVDDPLNLIHEKIIKAIGISQTANNNGEAVIHRDGGSSFDLILMDKEMPE 73
 DB 495 REVRILLVDNPNVLLVQKLLAVGFADTADTGEAA--LARMESTRYDMVFMDCQMPV 552
 QY 74 RDGVSTTKLRENEVKS-----MIVGVTSIADNEERAFMEAGLNHCLAKPLTKDKI 126
 DB 553 LDGYATRRWRAMETESGGRPVPIVANTAMAGDRERC-LAAGMDYLSKPVAREQL 609

RESULT 13
 Q8PJN8 PRELIMINARY; PRT; 1364 AA.
 AC Q8PJN8;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Two-component system sensor protein.
 GN XAC2492.
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furian L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Canavan F., Cardozo J., Chamberg F., Ciapina L.P.,
 RA Cicarilli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado N.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Weidman J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spínola L.A.F., Takita M.A., Tamara R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities";
 RL Nature 417:459-463(2002).
 DR EMBL: AE011687; AM37343.1; -
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR003661; His_kinA.
 DR InterPro: IPR005467; His_kinase.
 DR InterPro: IPR002570; Hpt.
 DR Pfam: PF02518; HATPase_C.1.
 DR Pfam: PF00512; HiskA.1.
 DR Pfam: PF01627; Hpt.1.
 DR Pfam: PF00989; PAS.2.
 DR Pfam: PF00072; response_reg.2.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR PRODOM: PD000039; Response_reg.2.
 DR TIGRFAITS: TIGR00229; sensory_box.2.
 DR PROSITE: PS00839; CHASE.1.
 DR PROSITE: PS0109; HIS_KIN.1.
 DR PROSITE: PS0113; PAC.2.
 DR PROSITE: PS0112; PAS.2.
 DR PROSITE: PS0110; RESPONSE_REGULATORY.2.
 KW Complete proteome.
 SQ SEQUENCE 1364 AA; 150282 MW; F7CCA3856B7E7165 CRC64;

Query Match 24.7%; Score 167.5; DB 16; Length 1364;
 Best Local Similarity 29.2%; Pred. No. 5e-06;
 Matches 35; Conservative 37; Mismatches 45; Indels 3; Gaps 2;

QY 17 NVLIVDDPLNLIHEKIIKAIGISQTANNNGEAVIHRDGGSSFDLILMDKEMPE 76
 DB 1033 LHLIVDDSDINCEVAQRILEGAMVTVADHSGQAVSTLKRAPNLFHLVMDVQMPVVDG 1092
 QY 77 VSTTKLRENEVKS--IVGVTSIADNEERAFMEAGLNHCLAKPLTKDKIPLINOLM 134
 DB 1093 YEATRLRLQIPALASLPVIALTAGAFRPQOEKA-LEAGNMGFIKPFNVVELVTAIRHFL 1151

RESULT 14
 Q85663 PRELIMINARY; PRT; 507 AA.
 AC Q85663;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE RSCC (Fragment).
 GN RSCC.
 OS Proteus mirabilis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Proteus.
 OX NCBI_TaxID=584;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BB2000;
 RX MEDLINE=99047557; PubMed=9829920;
 RA Belas R., Schneider R., Melch M.;
 RT "Characterization of Proteus mirabilis precocious swarming mutants:
 RT identification of tsbA, encoding a regulator of swarming behavior."

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RL J. Bacteriol. 180:6126-6139(1998).
CC -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
DR EMBL; AF071215; AAC82662.1; -.
DR HSSP; P06657; 2CHF.
DR InterPro; IPR003594; Atpbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pt_C.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HSKA; 1.
DR PRINTS; PD000039; Response_reg; 1.
DR PRODOM; PD000039; Response_reg; 1.
DR SMART; SM00386; HSKA; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
DR KINASE; Phosphorylation; Sensory transduction; Transferase.
KW NON_TER
FT 1
SQ SEQUENCE 507 AA; 57326 MW; F5DA2EAD9C35DEF5 CRC64;

Query Match 24.6%; Score 166.5; DB 2; Length 507;
Best Local Similarity 36.4%; Pred. No. 1.9e-06;
Matches 39; Conservative 26; Mismatches 39; Indels 3; Gaps 2;

QY 16 LNLVIVDDPLNLIHKKIKAIGISQTANNGBEAVIIHRDGGSSFDLILMDKEMPERD 75
Db LTVLIVDDHPINLLTDLQKIGENTATAEQCDALAFMQE--NHVDIILTDVNMPPNN 454

QY 76 GVSTTKKLEMEVKSMIVGVTSIADNEBERRAFMEAGLNHCLAKPLT 122
Db 455 GYQLATTVRELSSTIPIIGVTANATAAEKQRC-IDAGMNDVCVSPVS 500

RESULT 15
Q8P883 PRELIMINARY; PRT; 1364 AA.
AC Q8P883;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component system sensor protein.
GN XCC2360.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; Pubmed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Montello-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Chabergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Gregio C.C., Gruber A.,
RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
RL EMBL; AE012344; AAM41638.1; -.

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DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001789; Response_reg.
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DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00785; PAC; 2.
DR Pfam; PF00989; PAS; 2.
DR Pfam; PF00072; response_reg; 2.
DR PRINTS; PD000039; Response_reg; 2.
DR TIGRfam; TIGR00229; sensory_box; 2.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50113; PAC; 2.
DR PROSITE; PS50112; PAS; 2.
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KW Complete proteome.
SQ SEQUENCE 1364 AA; 150167 MW; 48F1C5FED9710316 CRC64;

Query Match 24.1%; Score 163.5; DB 16; Length 1364;
Best Local Similarity 30.3%; Pred. No. 1.1e-05;
Matches 36; Conservative 36; Mismatches 44; Indels 3; Gaps 3;

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QY 78 STTKKLEME-EVKSM-IVGVTSIADNEBERRAFMEAGLNHCLAKPLTDXDKIIPLINQLM 134
Db 1094 EATRRLRQPSLASLPVIALTAGAFRPOQEK-A-LEAGMNGFIKPFNVEELVTAIRHFL 1151

Search completed: August 14, 2003, 16:49:03
Job time : 98 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 19:06:41 ; Search time 41 Seconds
(without alignments)
526.508 Million cell updates/sec

Title: US-09-646-679-15
Perfect score: 678
Sequence: 1 MATKSMGDIKIKKLNVL.....LAKPLTKDKIPLINQLMDA 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	515	76.0	142	AAV42645	A. thaliana D22AT3
6	472	69.6	116	AAV42652	Brassica napus
7	437	64.5	104	AA10550	Arabidopsis thaliana
8	437	64.5	104	AA44440	Arabidopsis thaliana
9	301	44.4	70	AA10589	Arabidopsis thaliana

10	280	41.3	66	21	AA10590	Arabidopsis thaliana
11	213	31.4	71	21	AA10588	Arabidopsis thaliana
12	202	29.8	261	21	AA10588	Arabidopsis thaliana
13	192.5	28.4	67	20	AA10588	Arabidopsis thaliana
14	171.5	25.3	118	23	ABG70785	Brassica napus D22
15	156.5	23.1	471	24	AAO26983	Pseudomonas aeruginosa
16	156.5	23.1	496	24	AAO26995	Pseudomonas aeruginosa
17	156.5	23.1	666	24	AAO26994	Pseudomonas aeruginosa
18	156.5	23.1	709	24	AAO26993	Pseudomonas aeruginosa
19	156.5	23.1	719	24	AAO26992	Pseudomonas aeruginosa
20	156.5	23.1	802	24	AAO26991	Pseudomonas aeruginosa
21	156.5	23.1	870	24	AAO26990	Pseudomonas aeruginosa
22	156.5	23.1	887	24	AAO26989	Pseudomonas aeruginosa
23	156.5	23.1	900	24	AAO26987	Pseudomonas aeruginosa
24	156.5	23.1	906	24	AAO26986	Pseudomonas aeruginosa
25	156.5	23.1	931	24	AAO26985	Pseudomonas aeruginosa
26	156.5	23.1	922	24	AAO26984	Pseudomonas aeruginosa
27	155	22.9	922	24	AAO26983	Pseudomonas aeruginosa
28	149	22.0	1373	23	ABP73292	Histidine protein kinase
29	148.5	21.9	922	22	AAO26982	Histidine protein kinase
30	148.5	21.9	922	22	AAO26981	Histidine protein kinase
31	148.5	21.9	950	23	ABG93422	Herbicide-inducible protein
32	146	21.5	1018	21	AAO26980	Eucalyptus grandis
33	141	20.8	1146	20	AAO26979	Histidine kinase C
34	139.5	20.6	1281	20	AAO26978	os1 histidine kinase
35	139.5	20.6	1298	19	AAO26977	N. crassa os1p
36	139.5	20.6	1298	20	AAO26976	os1p amino acid synthase
37	139.5	20.6	1298	20	AAO26975	os1 histidine kinase
38	137	20.2	125	23	ABG70784	Yeast SUN1 receptor
39	134.5	19.8	1122	23	ABG92150	Herbicide-inducible protein
40	134	19.8	120	22	AAO26974	Putative P. abyssinicus
41	133.5	19.7	1023	22	ABG28668	Novel human diacylglycerol kinase-like
42	131	19.3	136	23	ABP31215	Human kinase-like
43	131	19.3	674	21	AAO26973	Human kinase-like
44	130	19.2	1081	20	AAO26972	Candida albicans S
45	130	19.2	1081	20	AAO26971	Candida albicans C

ALIGNMENTS

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ID AAV42637 standard; Protein; 136 AA.
AC AAV42637;
XX
XX
AC AAV42637;
XX
XX
DT 10-JAN-2000 (first entry)
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DE Brassica napus response regulator protein D22.
XX
XX
KW Signal transduction protein; dehiscence; male sterile plant; D22 gene; shatter resistance; oilseed rape; response regulator protein.
XX
XX
OS Brassica napus.
XX
XX
PN WO9949046-A1.
XX
XX
PD 30-SEP-1999.
XX
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PF 22-MAR-1999; 99WO-GB00905.
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PR 20-MAR-1998; 98GB-0006113.
XX
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PA (BIOG-) BIOGENMA UK LTD.
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PI Wyatt P, Roberts JA, Whitelaw C;
XX
XX
DR WPI; 1999-580449/49.
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DR N-ESDB; AAZ22974.
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PT A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants

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PD	O6-SEP-2000.	
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PR 13-AUG-1999; 99US-0148565.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150566.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 01-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 07-OCT-1999; 99US-0158028.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.4%; Score 538; DB 21; Length 142;
Best Local Similarity 78.9%; Pred. No. 4.7e-52;
Matches 112; Conservative 8; Mismatches 16; Indels 6; Gaps 2;

QY 1 MATKSMGDIEK-----IKKKL-NVLIIVDDDDPLNLIIEHKIKAIGGISTANGGEAVII 54
    ||||| | || :||| | ||||| | :||| | ||||| | ||||| |
Db 1 MATKSTGTGTEKTSIEVKKKLINLIIVDDDDPLNRLHEMIKIITGGISOTAKNGEEAVIL 60
    ||||| | || :||| | ||||| | :||| | ||||| | ||||| |
QY 55 HRDGGSSFDLILMDKEMPERGVSTTKKLEMEYKSMIVGVTSIADNEERRAFMEAGLN 114
    ||||| | || :||| | ||||| | :||| | ||||| | ||||| |
Db 61 HRDGEASFLLILMDKEMPERGVSTTKKLEMKVTSIMIVGVTSYADQEEERKAFMEAGLN 120
    ||||| | || :||| | ||||| | :||| | ||||| | ||||| |
QY 115 HCLAKPLTKDKIPLINOLMDA 136
    ||||| | || :||| | ||||| | :||| | ||||| | ||||| |
Db 121 HCLEKPLTKAKIFPLISHLEDA 142
    ||||| | || :||| | ||||| | :||| | ||||| | ||||| |

RESULT 5
AAV42645
ID AAY42645 standard; Protein; 142 AA.
XX AAY42645;
AC AAY42645;
XX 10-JAN-2000 (first entry)
DT 10-JAN-2000 (first entry)
XX A. thaliana DZ2AT3 putative peptide sequence.
DE A. thaliana DZ2AT3 putative peptide sequence.
XX Signal transduction protein; dehiscence; male sterile plant;
KW shatter resistance; oilseed rape; DZ2AT3 gene.
KW Arabidopsis thaliana.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX Key Location/Qualifiers
FH Misc-difference 57 /note= "unknown"
FT MISC-difference 88 /note= "unknown"
FT MISC-difference 88 /note= "unknown"
FT MISC-difference 88 /note= "unknown"
XX WO9949046-A1.
XX 30-SEP-1999.
XX 22-MAR-1999; 99WO-GB00905.
XX 20-MAR-1998; 98GB-0006113.
XX (BIOG-) BIOGEMMA UK LTD.
XX Wyatt P, Roberts JA, Whitelaw C;
XX WPI: 1999-580449/49.
XX N-PSDB: AAZ22978.
XX A nucleic acid encoding a signal transduction protein involved in plant
PT dehiscence, useful for producing shatter resistant male sterile plants
PT -
XX
XX Example 3; Fig 9; 71pp; English.
XX
XX The invention provides a nucleic acid encoding a signal transduction
CC protein involved in the process of dehiscence. The nucleic acids and
CC proteins are useful for regulating or controlling dehiscence of a pod or
CC an anther in a plant, useful in the production of male sterile plants.
CC The methods, etc. may be used in production of shatter resistance or
CC shatter-delayed plants such as oilseed rape (Brassica napus). The present
CC sequence represents a DZ2 A. thaliana homologue DZ2AT3 putative peptide
CC sequence.
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XX SQ Sequence 142 AA;
 Query Match 76.0%; Score 515; DB 20; Length 142;
 Best Local Similarity 76.1%; Pred. No. 1.7e-49;
 Matches 108; Conservative 8; Mismatches 20; Indels 6; Gaps 2;
 QY 1 MATKSMGDIK-----TKKL-NVLIIVDDPLNLIHKKIIGISQTANNKEEAVII 54
 DB 1 MATKSTGTEKTKIEVKKKLNVLIVDDPLNRLHEMIITIGISQTAKNGEEVIL 60
 QY 55 HRDGGSSFDLILMDKEMPERDGVSTTKKLEMEVKSMIVGVTSLADNEEERRAFWEAGLN 114
 DB 61 HRDGEASFDFLILMDKEMPERDGVSTTKKLEMEVKSMIVGVTSLADNEEERRAFWEAGLN 120
 QY 115 HCLAKPLTKDKIPLINOLMDA 136
 DB 121 HCLEKPLTKAKIFPLISHLEDA 142
 RESULT 6
 AAY42652
 ID AAY42652 standard; Protein; 116 AA.
 AC AAY42652;
 DT 10-JAN-2000 (first entry)
 DE Brassica response regulator' protein D22B putative peptide sequence.
 KW Signal transduction protein; dehiscence; male sterile plant; D22B gene;
 KW shatter resistance; oilseed rape; response regulator protein.
 OS Brassica napus.
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "unknown"
 PN WO9949046-A1.
 XX 30-SEP-1999.
 PF 22-MAR-1999; 99WO-GB00905.
 XX 20-MAR-1998; 98GB-0006113.
 PR (BIOG-) BIOGEMMA UK LTD.
 PA Wyatt P, Roberts JA, Whitelaw C;
 PI WPI: 1999-580449/49.
 DR N-PSDB; AAZ22976.
 XX A nucleic acid encoding a signal transduction protein involved in plant
 PT dehiscence, useful for producing shatter resistant male sterile plants
 PT -
 XX Example 2; Fig 6; 71pp; English.
 CC The invention provides a nucleic acid encoding a signal transduction
 CC protein involved in the process of dehiscence. The nucleic acids and
 CC proteins are useful for regulating or controlling dehiscence of a pod or
 CC an anther in a plant, useful in the production of male sterile plants.
 CC The methods, etc. may be used in production of shatter resistance or
 CC shatter-delayed plants such as oilseed rape (Brassica napus). The present
 CC sequence represents the B. napus D22B putative peptide sequence.
 XX Sequence 116 AA;
 Query Match 69.6%; Score 472; DB 20; Length 116;
 Best Local Similarity 80.2%; Pred. No. 8.4e-45;
 Matches 93; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 21 YDDPLNLIHKKIIGISQTANNKEEAVIIHRDGGSSFDLILMDKEMPERDGVSTT 80
 DB 1 YXDDFVIRKLHEIIIIKIGISQTAKNGEEAVNIHRDGNASFDLILMDKEMPERDGLSAT 60
 QY 81 KKLREMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPLTKDKIPLINOLMDA 136
 DB 61 KKLREMKVTSIIIGVTTLADNEEERKAFMEAGLNHCLAKPLSKAKIPLINOLMDA 116
 RESULT 7
 AAG10350
 ID AAG10350 standard; Protein; 104 AA.
 AC AAG10350;
 DT 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 8917.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 XX 06-SEP-2000.
 PF 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 08-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126284.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
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 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132407.
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 PR 06-MAY-1999; 99US-0132485.
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 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.

PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
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PR	18-JUN-1999;	99US-0139492.
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PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140354.
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PR	29-JUN-1999;	99US-0140901.
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PR	02-JUL-1999;	99US-0142055.
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PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	26-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	30-AUG-1999;	99US-0151080.
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PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
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PR	29-OCT-1999;	99US-0162142.
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Best Local Similarity 84.5%; Pred. No. 5.9e-41;		
Matches 87; Conservative 6; Mismatches 10; Indels 0; Gaps 0;		
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QY 94 GVTSLADNEERAFMEAGLNHCLAKPLTKDKIILINOLMDA 136
D6 62 GVTSAOEEERAFMEAGLNHCLAKPLTKAKIFPLSHLFDA 104

RESULT 8
ID AAG44440 standard; Protein; 104 AA.
XX AAG44440;
AC AAG44440;
XX
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 55669.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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22-JUL-1999; 99US-0145089.
23-JUL-1999; 99US-0145192.
23-JUL-1999; 99US-0145145.
23-JUL-1999; 99US-0145218.
23-JUL-1999; 99US-0145224.
26-JUL-1999; 99US-0145276.
27-JUL-1999; 99US-0145913.
27-JUL-1999; 99US-0145918.
27-JUL-1999; 99US-0145919.
28-JUL-1999; 99US-0145951.
02-AUG-1999; 99US-0146386.
02-AUG-1999; 99US-0146388.
02-AUG-1999; 99US-0146389.
03-AUG-1999; 99US-0147036.
04-AUG-1999; 99US-0147204.
04-AUG-1999; 99US-0147302.
05-AUG-1999; 99US-0147192.
05-AUG-1999; 99US-0147260.
06-AUG-1999; 99US-0147303.
06-AUG-1999; 99US-0147416.
09-AUG-1999; 99US-0147493.
09-AUG-1999; 99US-0147935.
10-AUG-1999; 99US-0148171.
11-AUG-1999; 99US-0148319.
12-AUG-1999; 99US-0148341.

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 RESULT 9
 AAG21089
 ID AAG21089 standard; Protein; 70 AA.
 XX
 AC AAG21089;
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23518.
 XX
 KW Protein identification; signal transduction pathway; met
 KW hybridisation assay; genetic mapping; gene expression co
 KW termination sequence.
 KW
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PE 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
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 PR 04-MAY-1999; 99US-0132048.
 PR 05-MAY-1999; 99US-0132407.
 PR 06-MAY-1999; 99US-0132484.
 PR 07-MAY-1999; 99US-0132863.
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 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
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 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.

[illegible]

RESULT 10
AAG21090
ID AAG21090 standard; Protein; 66 AA.
XX
AC AAG21090;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23519.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
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PR 07-MAY-1999; 99US-0132487.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139463.
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PR 18-JUN-1999; 99US-0139763.
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PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144331.
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PR 20-JUL-1999; 99US-0144632.
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PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147935.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.

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PR	25-AUG-1999;	99US-0150566.	XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 23517.
PR	26-AUG-1999;	99US-0150884.	XX	DE	
PR	27-AUG-1999;	99US-0151065.	XX	DE	
PR	27-AUG-1999;	99US-0151066.	XX	DE	
PR	27-AUG-1999;	99US-0151080.	XX	DE	
PR	27-AUG-1999;	99US-0151303.	XX	DE	
PR	30-AUG-1999;	99US-0151438.	XX	DE	
PR	31-AUG-1999;	99US-0151438.	XX	DE	
PR	01-SEP-1999;	99US-0151930.	XX	DE	
PR	07-SEP-1999;	99US-0152363.	XX	DE	
PR	10-SEP-1999;	99US-0153070.	XX	DE	
PR	13-SEP-1999;	99US-0153758.	XX	DE	
PR	15-SEP-1999;	99US-0154018.	XX	DE	
PR	16-SEP-1999;	99US-0154039.	XX	DE	
PR	20-SEP-1999;	99US-0154779.	XX	DE	
PR	22-SEP-1999;	99US-0155139.	XX	DE	
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PR	04-OCT-1999;	99US-0157117.	XX	DE	
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PR	21-OCT-1999;	99US-0160741.	XX	DE	
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PR	28-OCT-1999;	99US-0162142.	XX	DE	
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Db	1 MPERDGVSTTKLRNEMVKSMTIVGYTSLADNDEEERAEAGLNHCLAKPLTKDKIPLI 60		XX	AC	
QY	131 NOLMDA 136		XX	AC	
Db	61 SHLFA 66		XX	AC	
RESULT 11			XX	AC	
AAG21088			XX	AC	

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Best Local Similarity 84.8%; Pred. No. 1.1e-23;
Matches 56; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
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PR 19-JUL-1999; 99US-0144331.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
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PR 22-JUL-1999; 99US-0145192.
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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
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PR 06-AUG-1999; 99US-0147303.
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PR 16-AUG-1999; 99US-0149368.
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PR 25-AUG-1999; 99US-0150366.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159329.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161992.
PR 29-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 31.4%; Score 213; DB 21; Length 71;
Best Local Similarity 73.4%; Pred. No. 3.7e-16;
Matches 47; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

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Db 1 MATKSTGTGTEKTSIEVKKKLINVLIVDDDPNRLHEMIKTIIGGISQAKNGEEAVIL 60
QY 55 HRDG 58
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Db 61 HRDG 64

RESULT 12
AAB25159
ID AAB25159 standard; Protein; 261 AA.
XX
AC AAB25159;

XX 15-MAR-2001; 2001JP-0073812.
 PR 29-JUN-2001; 2001JP-0198639.
 PR 29-JUN-2001; 2001JP-0198640.
 XX (SUMO) SUMITOMO CHEM CO LTD.
 XX Kakiimoto T, Higuchi M, Inoue T;
 PI WPI; 2002-693041/75.
 DR
 XX
 XX Analyzing agonist or antagonist activity of a substance for use as a
 PT plant growth regulator, comprises measuring intracellular signal
 PT transduction from a cytokinin receptor expressed in a cell contacted
 PT with the test substance -
 XX
 XX Disclosure; Page 42; 47pp; English.
 XX
 CC The invention discloses a method for analysing antagonist or agonist
 CC activity to a cytokinin receptor. The method comprises bringing a
 CC candidate substance into contact with a transformed cell, in which a DNA
 CC encoding the receptor has been introduced, and then measuring the
 CC existence, or the quantity, of the intracellular signal transduction from
 CC the receptor expressed in the cell. The cytokinin receptor comprises an
 CC extracellular region of the receptor, transmembrane regions, a histidine
 CC kinase region and a receiver region of the kinase. The transmembrane
 CC regions and kinase region are homogeneous to each other and the receptor
 CC region is heterogeneous to them. Cytokinins are plant hormones relevant
 CC to cell division and differentiation of higher plants. The method is used
 CC for analysing agonist or antagonist activity to a cytokine receptor. A
 CC substance with agonist or antagonist activity to the receptor can be
 CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
 CC The advantage is that the candidate substances do not need to be prepared
 CC in such large amounts as in previous methods and that the method avoids
 CC the immensely long time to observe and evaluate the growth of the plant
 CC and the physiological changes of the plant after spraying. The sequence
 CC presented is the E. coli receiver region of histidine kinase which can
 CC transmit signals to the cytokinin receptor.
 XX
 XX Sequence 118 AA;
 SQ
 Query Match 25.3%; Score 171.5; DB 23; Length 118;
 Best Local Similarity 33.9%; Pred. No. 3.2e-11;
 Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;
 QY 18 VLIVDDPLNLIIEKIIKAIGISQTANNGEAVIIHRDGGSPDLILMDKEMPERDGV 77
 DB 6 ILVVDHPINERLLADQLGSLGQCKTANDGVDALNVL--SKNHIDIVLSVNNPMDGY 63
 QY 78 STTKKLEMEVKSMIVGVTSLADNEEERAFMEAGLNHCLAKPLTKDKI 126
 DB 64 RLQRIQLGLTLPVIGVTANALAEKQRC-LESGMDLSLSKRPVTLDWI 111
 RESULT 15
 AAO26983
 ID AAO26983 standard; Protein: 471 AA.
 XX
 XX AAO26983;
 AC
 XX
 XX 10-MAY-2003 (first entry)
 DT
 XX Pseudomonas aeruginosa PvrR related protein, SEQ ID NO 4.
 DE
 XX Antibacterial; PvrR; variant Pseudomonas; microorganism; gram negative;
 KW phenotype-mediated antibiotic-resistance; microorganism; gram negative;
 KW bacterial infection.
 XX
 XX Pseudomonas aeruginosa.
 OS
 XX WO2003004691-A2.
 PN
 XX 16-JAN-2003.
 PD

XX 05-JUL-2002; 2002WO-US23242.
 XX
 XX 06-JUL-2001; 2001US-303286P.
 PR 16-APR-2002; 2002US-373233P.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 PA
 XX Ausubel FM, Drenkard E;
 PI
 XX WPI; 2003-221608/21.
 DR N-PSDB; AAL55304.
 XX
 XX New isolated PvrR polypeptide and polynucleotide that regulates
 PT bacterial biofilm formation, useful for the diagnosis, prevention and
 PT treatment of gram-negative or gram-positive bacterial infection -
 XX
 XX Disclosure; Fig 5E; 185pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide comprising a PvrR
 CC (variant Pseudomonas) amino acid sequence having at least 50 % identity
 CC to a 399 residue amino acid sequence, given in the specification, where
 CC expression of the polypeptide, in a microorganism, affects phenotype-
 CC mediated antibiotic-resistance in the microorganism. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and treatment of gram negative or gram-positive bacterial
 CC infection. This sequence represents a Pseudomonas protein used in the
 CC exemplification of the invention.
 XX
 XX Sequence 471 AA;
 SQ
 Query Match 23.1%; Score 156.5; DB 24; Length 471;
 Best Local Similarity 35.8%; Pred. No. 9.9e-09;
 Matches 38; Conservative 22; Mismatches 43; Indels 3; Gaps 3;
 QY 16 LNVLVDDPLNLIIEKIIKAIGISQTANNGEAVIIHRDGGSPDLILMDKEMPERD 75
 DB 352 LRVLVVEDRAINQLILRDOMEALGCVSELLFDGREA-LLRQC-TACFDVLTIDINMPNMN 409
 QY 76 GVSTTKKLEMEVKSMIVGVTSLADNEEERAFMEAGLNHCLAKPL 121
 DB 410 GYELTAEELRRQGFQPIIGATANAMREERERC-MSAGMNDCLVRPV 454
 Search completed: August 13, 2003, 19:11:13
 Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 19:10:32 : Search time 17 seconds
(without alignments)
338.487 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MATKSMGDIKIKKLNVL.....LAKPLTKDKRIPLINQLMDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	202	29.8	261	4	US-09-228-986-127
2	152.5	22.5	946	4	US-09-328-352-6073
3	150	22.1	1014	4	US-09-252-991A-22932
4	148	21.8	947	4	US-09-252-991A-22216
5	147	21.7	1627	4	US-09-252-991A-231677
6	145	21.4	1220	2	US-09-252-991A-20395
7	144	21.2	162	4	US-09-252-991A-20395
8	139.5	20.6	1281	2	US-08-843-530B-36
9	139.5	20.6	1298	2	US-08-843-530B-2
10	139.5	20.6	1298	2	US-08-843-530B-4
11	139.5	20.6	1298	2	US-08-843-530B-34
12	139.5	20.6	1441	4	US-09-252-991A-28143
13	138.5	20.4	234	4	US-09-634-238-220
14	135.5	20.0	760	4	US-09-252-991A-25928
15	135.5	20.0	860	4	US-09-252-991A-26112
16	133.5	19.7	918	2	US-08-843-530B-35
17	131	19.3	706	4	US-09-252-991A-18607
18	131	19.3	1036	4	US-09-252-991A-27075
19	130	19.2	1017	2	US-08-843-530B-18
20	130	19.2	1117	2	US-08-843-530B-33
21	127	18.7	506	4	US-09-252-991A-18168
22	125	18.4	227	4	US-09-107-532A-6769
23	124.5	18.4	133	4	US-09-328-352-5134
24	124	18.3	971	3	US-09-112-450-2
25	124	18.3	971	4	US-09-419-291A-2
26	124	18.3	2471	3	US-09-112-450-4
27	124	18.3	2471	4	US-09-419-291A-4

ALIGNMENTS

RESULT 1

US-09-228-986-127

; Sequence 127, Application US/09228986

; Patent No. 6359198

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

; FILE REFERENCE: 11000/1020

; CURRENT APPLICATION NUMBER: US/09/228,986

; CURRENT FILING DATE: 1999-01-12

; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: fastseq for Windows Version 3.0

; SEQ ID NO 127

; LENGTH: 261

; TYPE: PRT

; ORGANISM: Pinus radiata

US-09-228-986-127

Query Match 29.8%; Score 202; DB 4; Length 261;

Best Local Similarity 36.5%; Pred. No. 7e-16; Mismatches 37; Indels 2; Gaps 2;

Matches 42; Conservative 34; Mismatches 37; Indels 2; Gaps 2;

QY 18 VLIVDDPLNLIIHEKIIKAIGGISQTANGEEAVIHRDGGSSFDILMDKEMPERDGV 77

Db 137 ILLVEDTQINRIIFGRVLQSLNLYCEEAEKGVADYFKQ-GRTYDVLMDKEMPVMDGH 195

QY 78 STTKKLREMEYKSMIVGVTSADNEERRAEAGLNHCLAKPLTKDKIIPINQ 132

Db 196 EATRLRSRGVATPIVALTA-NTLQSDKDLTFEAGVDDFQSKPLSRDLVQLLQ 249

RESULT 2

US-09-328-352-6073

; Sequence 7973, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 7973

; LENGTH: 946

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-6073


```
Query Match      22.5%; Score 152.5; DB 4; Length 946;
Best Local Similarity 30.2%; Pred. No. 3.4e-09;
Matches 39; Conservative 34; Mismatches 41; Indels 15; Gaps 4;

QY 16 LNLVIVDDDDPLNLIHEKIIKAIGGISQTANNGEAVIHRDGGSS----FDLILMDKEM 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 674 LHILAVDDHLPNLIVLEALLGELNVKTKRALSQEQALNIQRIQDKLKPDLVFMDIQM 733
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 72 PERDGVSTTKKLEKEM-----EVKSMIVGVT--SLADNEEERRAFMEAGLNHCLAKPLTK 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 734 PVMSGIDTTRAIRSLESLTDGEMQLPIALTALHAD----EKQKLVGMNDYVTKPIQM 790
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 124 DKIIPLNQ 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 791 EQIIQILTQ 799
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
US-09-252-991A-31338
; Sequence 31338, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31338
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31338

Query Match      22.1%; Score 150; DB 4; Length 1014;
Best Local Similarity 25.5%; Pred. No. 7.4e-09;
Matches 35; Conservative 36; Mismatches 56; Indels 10; Gaps 4;

QY 2 ATKSMGDIKIK--KKNLVIVDDDDPLNLIHEKIIKAIGGISQTANNGEAVIHRDGG 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 868 ARSGVAEVEERKEARALSILLAEDHPFNRLTLTQLESGLHRVTSDEGEA--FERWQ 925
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 60 SSFDLILMDKEMPERDGVSTTKKLEMEV-----KSMIVGVTSLADNEEERRAFMEAGLN 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 926 EDFDVVITDGMPPRMDGYELARRISQEQALGRRRCRLVIALTASAKDALERC-LANGMD 984
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 HCLAKPLTKDKIPLIN 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 985 RVLFRPTLDELARLN 1001
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
US-09-252-991A-29359
; Sequence 29359, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
```

```
; SEQ ID NO 29359
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29359

Query Match      21.8%; Score 148; DB 4; Length 947;
Best Local Similarity 28.8%; Pred. No. 1.1e-08;
Matches 34; Conservative 33; Mismatches 43; Indels 8; Gaps 4;

QY 18 LLVIVDDDDPLNLIHEKIIKAIGGISQTANNGEAV-IHRDGGSSFDLILMDKEMPERDG 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 689 LLCVDNDNPANLLVQVLLSDIGAQTAVDSGYAALEVQRE---RFDLVFMDVQMPGMDG 745
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 77 VSTTKKLEMEVKSMI--VGVTSIADN--EEERRAFMEAGLNHCLAKPLTKDKIPLI 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 746 RQATEAIRWEAREVSPVPVIALTAHLSNKRALLQAGMDDYLTKTIDEQQLAQVV 803
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-252-991A-20395
; Sequence 20395, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20395
; LENGTH: 1627
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20395

Query Match      21.7%; Score 147; DB 4; Length 1627;
Best Local Similarity 31.9%; Pred. No. 3.3e-08;
Matches 37; Conservative 26; Mismatches 45; Indels 8; Gaps 3;

QY 14 KKNLVIVDDDDPLNLIHEKIIKAIGGISQTANNGEAVIHRDGGSSFDLILMDKEMPE 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1371 RELQVLVVDHNAVNRQLHQQLSLFGLHDVEEAENGLSALNLWH--GQPFDMVITDCHMPL 1428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 74 RDGVSTTKKLEMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKD 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1429 MSGSLARSIRQEERENGEPVWIIGLTADAQAPPEIERC-IOAGMNECLIKPIGLD 1483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-08-843-530B-36
; Sequence 36, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitreonikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; APPLICANT: Simon, Melvin I.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
```

[illegible]

```

Query Match      20.6% Score 139.5; DB 2; Length 1281;
Best Local Similarity 31.1%; Prec. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

Qy    2 ATKSMGDIKIKKKLVNLIVDDPLNLIHKEIKAIGGISOTANNNGEAV-IHRDGGG 60
Db    1075 ATPSLAD---NTKSP EILLASDNVNORLAKVILEYHHVTWVGNGEEAVEA---K 1128

Qy    61 SPDLILMDKEMPERGVSTTKKLREME-----VKSMIVGTYSLANEERERRAFMAGLNH 115
Db    1129 KFDVILMDVQPMINGGFATKIREYERSLGTSQRTPIALTAAH-MWGDRKCIQAOMDE 1187

Qy    116 CLAKPLTKDKIIPLI 130
Db    1188 YLSKPLQONHLIOTT 1202

RESULT 9
US-08-843-530B-2
; Sequence 2, Application US/08843530B
; Patent No. 593306
; GENERAL INFORMATION:
; APPLICANT: Selltreinnikoff, Claude
```

RESULT 9
US-08-843-530B-2
; Sequence 2, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-843-530B-4

Query Match 20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

QY 2 ATKSMGDIKIKKLNVLIVDDPLNLIIHEKIIKAIGISOTANNGEAV-IHRRDGS 60
DB 1075 ATPSLD---NTKSFLLAEDTVNQLAVKILEKHHVTVVNGGEAVEAVKR---K 1128

QY 61 SFDLILMDKEMPERDGVSTTKKUREME-----VKSMIVGVISLADNEERERAFMEAGLNH 115
DB 1129 KFDVILMDVQMPGGMGFATAKIERYSLSQRTPIALTATAH-MMGDRKKCIQAOMDE 1187

QY 116 CLAKPLTKDKIPLI 130
DB 1188 YLSKPLQNHLIQTI 1202

RESULT 11
US-08-843-530B-34
; Sequence 34, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; APPLICANT: Simon, Melvin I.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,530B
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1298 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-843-330B-34

Query Match          20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps 5;

QY 2 ATKSMGDIKIKKLNVLIVDDPLNLIHKEIKIKAIGISQTANNGEAV-IHRDGS 60
DB 1075 ATSLAD---NTKSFILLAEADNTVORLAVKILEXYHHVTVVGVNGEAVEAVR---K 1128
QY 61 SFDLILMDKEMPERDGVSTTKLREME----VKSMIVGVTSLADNEEERAFMEAGLNH 115
DB 1129 KFDVILMDVQPMGGEAFETAKREYERSLGSORTPIIALTAHA-MMGDREKCIQAQND 1187
QY 116 CLAKPLTKDKIPLI 130
DB 1188 YLSKPLQQNHLIQTI 1202

RESULT 12
US-09-252-991A-28143
; Sequence 28143, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28143
; LENGTH: 1441
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28143

Query Match          20.6%; Score 139.5; DB 4; Length 1441;
Best Local Similarity 28.8%; Pred. No. 2.2e-07;
Matches 34; Conservative 30; Mismatches 43; Indels 11; Gaps 3;

QY 16 LNVLIIVDDPLNLIHKEIKIKAIGISQTANNGEAVIHRDGGSSFDLILMDKEMPERD 75
DB 1182 VRLIIVDDNALNQVAEELSSSEGARVALADGGLAGVQQVLEASVPFDVAVLMDQMPPDID 1241
QY 76 GVSSTTKLRE-----NEVSMIVGVTSLADNEEERAFMEAGLNHCLAKPLTKDKII 127
DB 1242 GLEATRRIRADGRAGIPILANTAN-ASLAD----REACLAAGMNDHVAKPIDKERLV 1294

RESULT 13
US-09-634-238-220
; Sequence 220, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
```

```

; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.104301
; CURRENT APPLICATION NUMBER: US/09/634.238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-220

Query Match          20.4%; Score 138.5; DB 4; Length 234;
Best Local Similarity 30.2%; Pred. No. 2e-08;
Matches 35; Conservative 31; Mismatches 47; Indels 3; Gaps 2;

QY 18 VLIIVDDPLNLIHKEIKIKAIGISQTANNGEAVIHRDGGSSFDLILMDKEMPERDGV 77
DB 4 ILIVDEPAITLLOYNLEAEHYQVETATDQGEA--LDKVRSEPFDFILDLMLFSLSL 61
QY 78 STTKLREMEVKSVMIVGVTSLADNEEERAFMEAGLNHCLAKPLTKDKIPLINOL 133
DB 62 DVTCKINEEKIQTPIMILTA-KDNETDKIVGLEGADYVTRKPSPREIIARIKAI 116

RESULT 14
US-09-252-991A-25928
; Sequence 25928, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25928
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25928

Query Match          20.0%; Score 135.5; DB 4; Length 760;
Best Local Similarity 28.0%; Pred. No. 2.5e-07;
Matches 35; Conservative 31; Mismatches 54; Indels 5; Gaps 3;

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DB 612 QAAGDAAPVAAGQBIILVEDPNVQTVIEAMLSRSLGYRTLVADGIQAV--RSAERQYD 669
QY 64 LILMDKEMPERDGVSTTKLREMEVKSVMIVGVTSLADN--EEERRAFMEAGLNHCLAKPL 121
DB 670 AILMDCLPLVDGYSATREIRAQE-NGRQVPIIALTANALQDRENCIQAQMNDYLAKEPF 728

RESULT 15
US-09-252-991A-26112
; Sequence 26112, Application US/09252991A
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Thu Aug 14 17:18:20 2003

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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26112

Query Match      20.0%; Score 135.5; DB 4; Length 860;
Best Local Similarity 26.5%; Pred. No. 3e-07;
Matches 36; Conservative 35; Mismatches 56; Indels 9; Gaps 3;

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Db      722 IAPSSASDTTGEQRNTRVLLVEDNPVNLVAKGLLHKLGCQWIAEHGLNALKMLEE--H 779

QY      61 SFDLILMDKEMPERDGVSTTKLREM-----EVKSMIVGVTSIADNEFEERAFMEAGLNHC 116
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QY      117 LAKPLTKDKIPLINO 132
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Search completed: August 13, 2003, 19:13:02
Job time : 18 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2003, 19:12:22 : Search time 54 Seconds

(without alignments)
329,934 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MARKSGDIEKIKKLVLI.....LAKPLTKDKIPLINLMDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	202	29.8	261	15	US-10-101-464A-127
2	171.5	25.3	118	10	US-09-918-508-8
3	150	22.1	622	10	US-09-801-368-328
4	146	21.5	1018	15	US-10-101-464A-909
5	145	21.4	1220	10	US-09-801-368-332
6	143.5	21.2	712	10	US-09-801-368-336
7	137.5	20.3	974	15	US-10-136-120-2
8	137	20.2	125	10	US-09-918-508-7
9	132	19.5	1829	15	US-10-156-761-10049
10	128	18.9	1081	10	US-09-424-951-4
11	127.5	18.8	2150	14	US-10-135-322-17
12	126.5	18.7	207	9	US-09-815-242-11131
13	126	18.6	203	15	US-10-156-761-12532
14	125.5	18.5	227	15	US-10-156-761-9975
15	124.5	18.4	232	9	US-09-815-242-13783

16	124	18.3	971	14	US-10-116-048-2	Sequence 2, Appli
17	124	18.3	2471	14	US-10-116-048-4	Sequence 4, Appli
18	123.5	18.2	185	11	US-09-769-787-54	Sequence 54, Appl
19	123	18.1	1447	15	US-10-156-761-8624	Sequence 8624, Ap
20	122.5	18.1	248	15	US-10-156-761-12602	Sequence 12602, A
21	122.5	18.1	1044	15	US-10-101-464A-956	Sequence 956, App
22	122	18.0	248	9	US-09-815-242-12098	Sequence 12098, A
23	121.5	17.9	218	15	US-10-156-761-13746	Sequence 13746, A
24	120.5	17.8	222	9	US-09-815-242-11529	Sequence 11629, A
25	118.5	17.5	232	9	US-09-815-242-10420	Sequence 10420, A
26	118	17.4	890	15	US-10-101-464A-958	Sequence 958, App
27	118	17.4	1270	15	US-10-101-464A-979	Sequence 979, App
28	117.5	17.3	1173	14	US-10-135-322-19	Sequence 19, Appl
29	117.5	17.3	1176	10	US-09-918-508-2	Sequence 2, Appli
30	117	17.3	1383	15	US-10-156-761-13096	Sequence 13096, A
31	115	17.0	762	15	US-10-101-464A-114	Sequence 114, App
32	114.5	16.9	243	15	US-10-156-761-11581	Sequence 11581, A
33	113	16.7	747	12	US-10-100-294A-27	Sequence 27, Appl
34	112	16.5	228	15	US-10-156-761-10048	Sequence 10048, A
35	111.5	16.4	235	10	US-09-738-626-6370	Sequence 6370, Ap
36	111	16.4	669	11	US-09-918-508-4	Sequence 24, Appl
37	111	16.4	1036	10	US-09-918-508-4	Sequence 4, Appli
38	110.5	16.3	104	14	US-10-135-322-30	Sequence 30, Appl
39	110	16.2	573	11	US-09-819-143-10	Sequence 10, Appl
40	110	16.2	599	15	US-10-101-464A-117	Sequence 117, App
41	110	16.2	816	15	US-10-101-464A-827	Sequence 827, App
42	110	16.2	1240	15	US-10-101-464A-376	Sequence 976, App
43	109.5	16.2	100	14	US-10-135-322-29	Sequence 29, Appl
44	109.5	16.2	1092	14	US-10-135-322-18	Sequence 18, Appl
45	107	15.8	197	15	US-10-156-761-10458	Sequence 10458, A

ALIGNMENTS

RESULT 1

US-10-101-464A-127
; Sequence 127, Application US/10101464A
; Publication No. US20030045728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-10-101-464A-127

Query Match 29.8%; Score 202; DB 15; Length 261;
Best Local Similarity 36.5%; Pred. No. 4.4e-14;
Matches 42; Conservative 34; Mismatches 37; Indels 2; Gaps 2;

QY 18 VLIVDDPLNLIHKKIKAIGGTSOTANNEEAIVIHGGSSFDLLMKEMPERDGV 77

Db 137 ILLVDTQINRIIFGRVQLNLCYEEAENCKVAVDYFKQ-GRYDVLVMDKEMPYMDGH 195

QY 78 STTKKLREMEVKSMTVGVTSIADNDEERRAFMEAGLNHCLAKPLTKDKIPLINQ 132


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; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match 21.4%; Score 145; DB 10; Length 1220;
Best Local Similarity 29.0%; Pred. No. 6.6e-07;
Matches 40; Conservative 40; Mismatches 44; Indels 14; Gaps 6;

QY 8 DIEKIKKLNVLIVDDPLNLIIEKIIKA--IGGIS--QTANNGEA--VVIHRDGG 59
DB 1080 DDKNETSKILVVDNHNV---QEVIKRMLNLEGLENELACDGEADPKVELTSKG 1135
QY 60 SSFDILMDKEMPERDGVSTTKKL-REMEYKSMIVGTVSLADNEERARRAMEAGLNHCLA 118
DB 1136 ENYMFDMVQMPKVDGLSTKMIRROLGYTSPVALTAFADDSNIKEC-LESGMNGFLS 1194
QY 119 KPLTKDKIPLINQLMDA 136
DB 1195 KPDKRPRKLTILTEFCAA 1212

RESULT 6
US-09-801-368-366
; Sequence 366, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 366
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-366

Query Match 21.2%; Score 143.5; DB 10; Length 712;
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42; Indels 31; Gaps 3;

QY 10 EKIKKLNVLIVDDPLNLIIEKIIKAIGGISQTANNGEAAVVIHRDGGSSFDILMDK 69
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QY 70 EMPERDGVSTTKKLREMEYKS-----MIVGTVSLADN 101
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QY 102 EEERRAFMEAGLNHCLAKPL 121
DB 616 MDKRKALL-SGCNDYLTKPV 634

RESULT 7
US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Sakakibara, Hitoshi
; APPLICANT: Takei, Kentaro
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FAC
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match 20.3%; Score 137.5; DB 15; Length 974;
Best Local Similarity 24.6%; Pred. No. 3.2e-06;
Matches 35; Conservative 32; Mismatches 46; Indels 29; Gaps 3;

QY 17 NVLIIVDDPLNLIIEKIIKAIGGISQTANNGEAAVVI---HRDGGSSFDILMDKEMP 72
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RESULT 8
US-09-918-508-7
; Sequence 7, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
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; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match 21.4%; Score 145; DB 10; Length 1220;
Best Local Similarity 29.0%; Pred. No. 6.6e-07;
Matches 40; Conservative 40; Mismatches 44; Indels 14; Gaps 6;

QY 8 DIEKIKKLNVLIVDDPLNLIIEKIIKA--IGGIS--QTANNGEA--VVIHRDGG 59
DB 1080 DDKNETSKILVVDNHNV---QEVIKRMLNLEGLENELACDGEADPKVELTSKG 1135
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QY 119 KPLTKDKIPLINQLMDA 136
DB 1195 KPDKRPRKLTILTEFCAA 1212

RESULT 6
US-09-801-368-366
; Sequence 366, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 366
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-366

Query Match 21.2%; Score 143.5; DB 10; Length 712;
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42; Indels 31; Gaps 3;

QY 10 EKIKKLNVLIVDDPLNLIIEKIIKAIGGISQTANNGEAAVVIHRDGGSSFDILMDK 69
DB 498 EKVEPKINVLIVDDNVIQAILGSFLRKHKISKYKLAQNQEAVNIWKEGG--LHLIFMDL 555
QY 70 EMPERDGVSTTKKLREMEYKS-----MIVGTVSLADN 101
DB 556 QLPVLGIEAAKQIRDFKONGIGIOKSLNHSNLEKTSKRFSOAPVVIIVALTASNSQ 615
QY 102 EEERRAFMEAGLNHCLAKPL 121
DB 616 MDKRKALL-SGCNDYLTKPV 634

RESULT 7
US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Sakakibara, Hitoshi
; APPLICANT: Takei, Kentaro
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FAC
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match 20.3%; Score 137.5; DB 15; Length 974;
Best Local Similarity 24.6%; Pred. No. 3.2e-06;
Matches 35; Conservative 32; Mismatches 46; Indels 29; Gaps 3;

QY 17 NVLIIVDDPLNLIIEKIIKAIGGISQTANNGEAAVVI---HRDGGSSFDILMDKEMP 72
DB 830 NILVVDNKNVLRVAAALKKYGANVSCVESGKDAISLQPPHR-----EDACFMDVQMP 884
QY 73 ERDGVSTTKKLREMEYKSMIVGTVSLADNEERRA-----EWEAG 112
DB 885 EMDGFEATQIRQMELKANEERKNKLASIEGSTTAEYHLPVLAMTADVIQATYEECIKSG 944
QY 113 LNHCLAKPLTKDKIPLINQLM 134
DB 945 MDGYVSKPDEEQLYQAVSRLV 966

RESULT 8
US-09-918-508-7
; Sequence 7, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
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RESULT 12
US-09-815-242-11131
; Sequence 1131, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11131
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11131

Query Match      18.7%   Score 126.5;   DB 9;   Length 227;
Best Local Similarity 29.1%;   Pred. No. 6.7e-06;
Matches 34;   Conservative 30;   Mismatches 48;   Indels 5;   Gaps 2;

QY 18 VLVDDPLNLIHEKIIKAIGGISQTANNNGEEAVIIHRDGGSSFDLIIMDKEMPERGV 77
Db 4 LLLVDDDIETELSTLLELEGFVETANNGLAAL---QKLNESYKLVLLDVMMKPLNGI 60
QY 78 STTKKLREMEYKSMIVGVTSLADNEEBERRAFMEAGLNHCLAKPLTKDKIPLINOLM 134
Db 61 ETLKEIR--KVSNNPVMMLTARGEDIDRVGLGLEIGADDCLPKPFENDRELIARIKAIL 115

RESULT 13
US-10-156-761-12532
; Sequence 12532, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9975
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12532

Query Match      18.5%   Score 125.5;   DB 15;   Length 227;
Best Local Similarity 29.2%;   Pred. No. 8.6e-06;
Matches 38;   Conservative 28;   Mismatches 53;   Indels 11;   Gaps 5;

QY 10 EKIKKKLVNLIIVDDPLNLIHEKIIKAIG---GIS--QTANNNGEEAVIIHRDGGSSFDL 64
Db 4 EESRKPAPVVVADD---QTVVREGIVMLLGLLPGLIEYVGAAGDGHFAVKLVAE--LNPDV 58
QY 65 ILMDKEMPERDGVSTTKKLREMEYKSMIVGVTSLADNEEBERRAFMEAGLNHCLAKPLTKD 124
Db 59 VLMOLRMPRCDCVEATRRIRAEHPGTOVVVTVYADDESIFPA--LRAGARGYLTKDAGGD 117
QY 125 KIIPLINOLM 134
Db 118 EIVRAVESVL 127

RESULT 15
US-09-815-242-13783
; Sequence 13783, Application US/09815242
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; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12532
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12532

Query Match      18.6%   Score 126;   DB 15;   Length 203;
Best Local Similarity 29.5%;   Pred. No. 6.5e-06;
Matches 36;   Conservative 20;   Mismatches 46;   Indels 20;   Gaps 3;

QY 17 NVLIVDDPLNLIHEKIIKAIGGISQ--TANNNGEEAVIIHRDGGSSFDLIIMDKEMPER 74
Db 3 SVLVCDSDPLAREALRRVATVPGVERVTAAANGEE--VLRWGDADSDLIIMDVNMFGL 60
QY 75 DGVSTTKKLREMEYKSMIVGVTSLAD-----NEEBERRAFMEAGLNHCL 118
Db 61 GGVTVRLLSADPGARIIMLTVAEDLDGVALAARGAGLYLHKDASRAELRATVTQALA 120
QY 119 KP 120
Db 121 DP 122

RESULT 14
US-10-156-761-9975
; Sequence 9975, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9975
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9975

Query Match      18.5%   Score 125.5;   DB 15;   Length 227;
Best Local Similarity 29.2%;   Pred. No. 8.6e-06;
Matches 38;   Conservative 28;   Mismatches 53;   Indels 11;   Gaps 5;

QY 10 EKIKKKLVNLIIVDDPLNLIHEKIIKAIG---GIS--QTANNNGEEAVIIHRDGGSSFDL 64
Db 4 EESRKPAPVVVADD---QTVVREGIVMLLGLLPGLIEYVGAAGDGHFAVKLVAE--LNPDV 58
QY 65 ILMDKEMPERDGVSTTKKLREMEYKSMIVGVTSLADNEEBERRAFMEAGLNHCLAKPLTKD 124
Db 59 VLMOLRMPRCDCVEATRRIRAEHPGTOVVVTVYADDESIFPA--LRAGARGYLTKDAGGD 117
QY 125 KIIPLINOLM 134
Db 118 EIVRAVESVL 127

RESULT 15
US-09-815-242-13783
; Sequence 13783, Application US/09815242
```

Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13783
LENGTH: 232
TYPE: PRT
ORGANISM: Salmonella typhi
US-09-815-242-13783

Query Match 18.4%; Score 124.5; DB 9; Length 232;
Best Local Similarity 28.2%; Pred. No. 1.1e-05;
Matches 33; Conservative 31; Mismatches 48; Indels 5; Gaps 2;
QY 18 VLIYDDPDLNLIIEKIKAIIGISQTANNGEAVIHRDGGSSFDLILMDKEMPERDGV 77
DB 4 ILLYDDDDREITSLEKLEMEGFNLVADHGEQALELLOD---SIDLLDDVMPKNGI 60
QY 78 STTKKLEMEVKMIGVGTSLADNEEBERRAFMEAGLNHCLAKPLTKDKIPLINOLM 134
DB 61 DTLKALRQTHQTPVI--MLTARGNELDRVLGLGLGADDYLPKPFNDRELVARIRAIL 115

Search completed: August 13, 2003, 19:20:55
Job time : 55 secs

Qy	12	IKKKLVNLIIVDDPLNLIIHKEIKAIKGGISQTANNGEEAVIITHRDGSSFDLILMDKEM	71
Dd	955	LPEKLSILTADHPTRNLLKRLQNLLGYDDEATDGVA--LHKVSMQHYYDLITDVNM	1012
Qy	72	PERDGVSTTKKLREMEVKMSMIVGTSLADNEERRAFMEAGLNHCLAKPLTKDKIIPLIN	131
Dd	1013	PNVDFELTRKLREQNSLPWGLTANA-QANEREKGLNCGMNLCLFKPFLTDVLKTHLS	1071
Qy	132	QL 133	
Dd	1072	QL 1073	
RESULT 4			
C85879	probable sensor for regulator EvgA evgs [imported] - Escherichia coli (strain O157:H7)		
C:Species:	Escherichia coli		
C>Date:	16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001		
C:Accession:	C85879		
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Liller, L.; Grothbeck, E.J.; Davis, A.A.; Dimantal, E.; Potamocousis, K.; Nature 409, 529-533, 2001			
A>Title:	Genome sequence of enterohemorrhagic Escherichia coli O157:H7.		
A:Reference number:	AB5480; MUID:21074935; PMID:11206951		
A:Accession:	C85879		
A>Status:	preliminary		
A:Molecule type:	DNA		
A:Residues:	1-1197 <STO>		
A:Cross-references:	GB:AE005174; NID:g12516740; PIDN:AAG57495.1; GSPOB:GN00145		
A:Experimental source:	strain O157:H7, substrain EDL933		
C:Genetics:			
C:Superfamily:	evgs protein; response regulator homology		
Query Match	26.0%;	Score 176.5;	DB 2; Length 1197;
Best Local Similarity	34.4%;	Pred. No. 7.5e-07;	
Matches	42;	Conservative 25;	Mismatches 52; Indels 3; Gaps
Qy	12	IKKKLVNLIIVDDPLNLIIHKEIKAIKGGISQTANNGEEAVIITHRDGSSFDLILMDKEM	71
Dd	955	LPEKLSILTADHPTRNLLKRLQNLLGYDDEATDGVA--LHKVSMQHYYDLITDVNM	1012
Qy	72	PERDGVSTTKKLREMEVKMSMIVGTSLADNEERRAFMEAGLNHCLAKPLTKDKIIPLIN	131
Dd	1013	PNVDFELTRKLREQNSLPWGLTANA-QANEREKGLNCGMNLCLFKPFLTDVLKTHLS	1071
Qy	132	QL 133	
Dd	1072	QL 1073	
RESULT 5			
H87640	sensor histidine kinase/response regulator [imported] - Caulobacter crescentus		
C:Species:	Caulobacter crescentus		
C>Date:	20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001		
C:Accession:	H87640		
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidgen, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.N., Jr.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001			
A>Title:	Complete Genome Sequence of Caulobacter crescentus.		
A:Reference number:	AB87249; MUID:21173698; PMID:11259647		
A:Accession:	H87640		
A>Status:	preliminary		
A:Molecule type:	DNA		
A:Residues:	1-394 <STO>		
A:Cross-references:	GB:AE005673; NID:g3324832; PIDN:AAK25124.1; GSPOB:GN00148		
C:Genetics:			
C:Gene:	CC3162		

Query Match
25.7%; · Score 174; DB 2; Length 394;

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Best Local Similarity 31.7%; Pred. No. 3.4e-07;
Matches 39; Conservative 31; Mismatches 49; Indels 4; Gaps 2;

QY 14 KLVNVLVDDPLNLIIEHKIIKAIGGISQTANNGEAVIIHRDGGSSFDLILMKEMPE 73
Db 262 RSHILIVDDNATNRVWALCMFECTSEGVADGVEAVEMARG--RFDLILMKMPR 319
QY 74 RGVSTTKLREMEVKSMIVGTVSLADNEE--ERRAFMEAGLNHCLAKPLTKDKI 131
Db 320 MDGVAATRAIRELSGRSSAAPVALTANADPADVHTYLAAGQDVKPERIALVLN 379
QY 132 QLM 134
Db 380 SLL 382

RESULT 6
AD0790
Sensor protein RscC (EC 2.7.3.-) [imported] - Salmonella enterica subsp. enterica serovar
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AD0790
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-948 <FAR>
A:Cross-references: GB:AL513382; PIDN:CAD07502.1; PID:gl6503497; GSPDB:GN00176
C:Genetics:
A:Gene: rscC
A:Superfamily: rscC protein; response regulator homology
C:Keywords: phosphotransferase

Query Match 25.6%; Score 173.5; DB 2; Length 948;
Best Local Similarity 33.9%; Pred. No. 1e-06;
Matches 37; Conservative 33; Mismatches 36; Indels 3; Gaps 2;

QY 18 VLIVDDPLNLIIEHKIIKAIGGISQTANNGEAVIIHRDGGSSFDLILMKEMPERDV 77
Db 827 ILVVDHPINRLLADQLGSLGYQCKTANDGVDALNVL--SKNAIDIVLSDVNMENMDGY 884
QY 78 STTKKLREMEVKSMIVGTVSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
Db 885 RLQTRIQRLGLTLPVIGVTANALAEKQRC-LESQMDSCLSKPVTLDAL 932

RESULT 7
BVECCC
sensor protein rscC (EC 2.7.3.-) - Escherichia coli (strain K-12)
N:Alternate names: regulatory protein rscC
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002
C:Accession: H64991; J00069; A48659
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64991
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-933 <BLAT>
A:Cross-references: GB:AE00311; GB:U00096; NID:gl788547; PIDN:AA075278.1; PID:gl788548;
A:Experimental source: strain K-12, substrain MG1655
R:Stout, V.; Gottesman, S.
J. Bacteriol. 172, 659-669, 1990

A:Title: RcsB and RcsC: a two-component regulator of capsule synthesis in Escherichia
A:Reference number: J00069; MUID:90130299; PMID:2404948
A:Accession: J00069
A:Molecule type: DNA
A:Residues: 1-112, 'IG', 115-918, 'S', 920-933 <STO>
A:Cross-references: GB:M28242; NID:gl47524; PIDN:AAA24503.1; PID:gl47525
A:Experimental source: strain K12
R:Jayaratne, P.; Keenleyside, W.J.; MacLachlan, P.R.; Dodgson, C.; Whitfield, C.
J. Bacteriol. 175, 5384-5394, 1993
A:Title: Characterization of rcsB and rcsC from Escherichia coli O9: K30:H12 and exar
A:Reference number: A48659; MUID:93374832; PMID:8366025
A:Accession: A48659
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-112, 'IG', 115-298, 'V', 300-759, 'E', 761-873, 'T', 875-921, 'V', 923-931, 'E', 9
A:Cross-references: GB:LL1272; NID:gl47527; PIDN:AAA24505.1; PID:gl47528
A:Experimental source: strain K30 (O9:K30:H12)
C:Comment: This protein acts as the sensor of the two-component regulatory system to
C:Genetics:
A:Gene: rscC
A:Map position: 48 min
A:Superfamily: rscC protein; response regulator homology
C:Keywords: autophosphorylation; capsule synthesis; phosphohistidine; phosphoprotein.
F:4-26/Domain: transmembrane #status predicted <TM1>
F:298-318/Domain: transmembrane #status predicted <TM2>
F:811-920/Domain: response regulator homology <RRH>
F:463/Binding site: phosphate (His) (covalent) #status predicted
F:859/Binding site: phosphate (asp) (covalent) #status predicted

Query Match 25.3%; Score 171.5; DB 1; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.5e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 VLIVDDPLNLIIEHKIIKAIGGISQTANNGEAVIIHRDGGSSFDLILMKEMPERDV 77
Db 811 ILVVDHPINRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMENMDGY 868
QY 78 STTKKLREMEVKSMIVGTVSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
Db 869 RLQTRIQRLGLTLPVIGVTANALAEKQRC-LESQMDSCLSKPVTLDVI 916

RESULT 8
C91017
sensor for ctr capsule biosynthesis [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: C91017
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, (
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
A:Reference number: A99629; MUID:21156231; PMID:11238796
A:Accession: C91017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-933 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036530.1; PID:gl3362576; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS107
C:Superfamily: rscC protein; response regulator homology

Query Match 25.3%; Score 171.5; DB 2; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.5e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 VLIVDDPLNLIIEHKIIKAIGGISQTANNGEAVIIHRDGGSSFDLILMKEMPERDV 77
Db 811 ILVVDHPINRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMENMDGY 868
QY 78 STTKKLREMEVKSMIVGTVSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
```

Db 869 RLTORIRQLGLTLPVIGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 916

RESULT 9

E85861

Hypothetical protein rscC [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: E85861

R:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 523-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85861

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-933 <STO>

A:Cross-references: GB:AE005174; NID:q12516556; PIDN:AAG57353.1; GSPDB:GN00145; UWGP:Z34

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

C:Superfamily: rscC protein; response regulator homology

Query Match 25.3%; Score 171.5; DB 2; Length 933;

Best Local Similarity 33.9%; Pred. No. 1.5e-06;

Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 LVIVDDPLNLIIEHKIKAIGGISOQTANNGEEAVIIHRDGGSFLLIMDKEMPERDGV 77

DB 811 ILVDDHPINRLADQLGSGYQCKTANDGVDAINVL--SKNHIDVLSDVNPNDGV 868

QY 78 STTKKLEMEVKSMIVGVTSLADNEERRAFMEAGLNHCLAKPLTKDKI 126

DB 869 RLTORIRQLGLTLPVIGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 916

RESULT 10

AD0149

Two component sensor kinase/response regulator protein RscC (EC 2.7.3.-) [imported] - Yersinia pestis

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C:Accession: AD0149

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AD0149

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-957 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC90055.1; PID:g15979276; GSPDB:GN00175

A:Gene: rscC

C:Superfamily: rscC protein; response regulator homology

C:Keywords: phosphotransferase

Query Match 25.3%; Score 171.5; DB 2; Length 957;

Best Local Similarity 35.1%; Pred. No. 1.5e-06;

Matches 39; Conservative 29; Mismatches 40; Indels 3; Gaps 2;

QY 16 LNVIVDDPLNLIIEHKIKAIGGISOQTANNGEEAVIIHRDGGSFLLIMDKEMPERD 75

DB 835 LQILVDDHPINRLADQLTGLYEVITANDGLDALVALNT--NTVDMVLTDVNMNMD 892

QY 76 GVSTTKKLEMEVKSMIVGVTSLADNEERRAFMEAGLNHCLAKPLTKDKI 126

DB 893 GYRLTERLQNLNHPFIIGVTANALAEKQRC-IEAGMDCLSKPVTLDTL 942

RESULT 11

E87644

Sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: E87644

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko, n.; J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87644

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-642 <STO>

A:Cross-references: GB:AE005673; NID:g13424865; PIDN:AAK25153.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3191

Query Match 24.0%; Score 162.5; DB 2; Length 642;

Best Local Similarity 33.0%; Pred. No. 5.5e-06;

Matches 36; Conservative 28; Mismatches 40; Indels 5; Gaps 2;

QY 16 LNVIVDDPLNLIIEHKIKAIGGISOQTANNGEEAVIIHRDGGSFLLIMDKEMPERD 75

DB 514 LVLLVEDNATRLTATRMLEALGARVTTAEDCAQGVAAARQG---FDLILMDIQMPVMD 570

QY 76 GVSTTKKLEMEVKSMIVGVTSLADN--EERRAFMEAGLNHCLAKPLT 122

DB 571 GVEATHIRAFNSPAGAAPTILANTANAMAHQAQSYLAAGMDGAIAKPLS 619

RESULT 12

AD0432

Aerobic respiration control sensor/response regulatory protein (EC 2.7.3.-) [imported]

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C:Accession: AD0432

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AD0432

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-778 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92784.1; PID:g15981477; GSPDB:GN00175

A:Gene: arcB

C:Superfamily: aerobic respiration control sensor protein arcB; response regulator ho

C:Keywords: phosphotransferase

Query Match 24.0%; Score 162.5; DB 2; Length 778;

Best Local Similarity 27.0%; Pred. No. 6.8e-06;

Matches 33; Conservative 38; Mismatches 48; Indels 3; Gaps 2;

QY 16 LNVIVDDPLNLIIEHKIKAIGGISOQTANNGEEAVIIHRDGGSFLLIMDKEMPERD 75

DB 525 LVLLVEDIELNVIVARSVLKLGNSVDVANNGHDALAMFN--EEDFDLVLLDIQLPDMS 582

QY 76 GVSTTKKLEMEVKSMIVGVTSLADNE--EERRAFMEAGLNHCLAKPLTKDKIPLINOLM 134

DB 583 GLDIARQIRAEYKGKSLPPLVALTANVLKDKKEYLDAGMDVLSKPLSVFALTAMIKQFW 642

QY 135 DA 136

DB 643 DS 644

RESULT 13

A69487

response regulator homclog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Mar-2003
C:Accession: A69487
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L. Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A:Reference number: A69250; MUID:98043343; PMID:9389475
A:Accession: A69487
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <KLS>
A:Cross-references: GB:AE000971; GB:AE000782; NID:g2689294; PIDN:AA89351.1; PID:g264864
C:Superfamily: signal transduction receiver (phosphoacceptor) protein (CheY-like); respC
C:Keywords: phosphoprotein
F:4-110/Domain: response regulator homology <RRH>
F:50/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 23.5%; Score 159; DB 2; Length 117;
Best Local Similarity 28.3%; Pred. No. 1.5e-06;
Matches 36; Conservative 42; Mismatches 31; Indels 18; Gaps 5;

QY 16 LNVLVDD-----DPLNLIHE-KIIRKAIGGISOTANNGEAVIIHRDGGSSFDLILMDK 69
DB 2 IKVWVDDIEAKRILMKDKYVIE-----ASNGREAVELYRE--ERPDVILMDV 51
QY 70 EMPERDGVSTYKTKLREMEVKSMIVGVTSLADNEERAFMEAGLNHCLAKPLTKDKIPL 129
DB 52 MNPMLNGIEATSEIKKIDPAKIVATAYASSKGEK--VIEAGADYILKPFTRKEVVEL 109
QY 130 INQLMDA 136
DB 110 IKRILNS 116

RESULT 14

C82151
sensor histidine kinase VC1831 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82151
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B. Nature 405, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82151
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-736 <HEI>
A:Cross-references: GB:AE004259; GB:AE003852; NID:g9656353; PIDN:AAF94979.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El for
C:Genetics:
A:Gene: VC1831
A:Map position: 1

Query Match 23.5%; Score 159; DB 2; Length 736;
Best Local Similarity 30.8%; Pred. No. 1.3e-05;
Matches 41; Conservative 35; Mismatches 45; Indels 12; Gaps 5;

QY 8 DIEKIKK---LNVLVDDPLNLIHEKIIRKAIGGISOTANNGEAVIIHRDGGSSFD 63
DB 590 DVKPTAKTYPLGLRVLIVEDNRTNIMLEAFMRNKFECHSMDGVQAITALQE--SSFD 647
QY 64 LILMDKEMPERDGVSTTKLREK---EYKSMIVGVTSLAD-NEERAFMEAGLNHCLAK 119
DB 648 LVLMNDHMLPKDGIQTROIPLPQAKILLFGCT--ADVFKDTRDKMLSGAGADDDIAK 705

QY 120 PLTRDKIIPLIHQ 132
DB 706 PIAHELDMALEQ 718

RESULT 15

AG1897
two-component hybrid sensor and regulator all0729 [imported] - Nostoc sp. (strain PCC C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG1897
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1645 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072686.1; PID:g17130074; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0729

Query Match 23.5%; Score 159; DB 2; Length 1645;
Best Local Similarity 27.7%; Pred. No. 3.1e-05;
Matches 39; Conservative 40; Mismatches 50; Indels 12; Gaps 3;

QY 3 TKSMGDIKIKKLNVLIVDDPLNLIHEKIIRKAIGGISOTANNGEAVIIHRDGGSSF 62
DB 1414 TRSVIGLAPQOQRECRILVDDVADSRLLVLLSSGVGVQEAANGQEAALAIWQWHP-- 1471
QY 63 DLILMDKEMPERDGVSTTKLREMEVK-----SMIVGVTSLADNEERAFMEAGL 113
DB 1472 QLILMDMRPIMDGYEATHFIRSAEINHTTIPNPHITIIALTAAH--FEQROAMLVQVC 1530
QY 114 NHCLAKPLTKDKIIPLIHQ 134
DB 1531 DDLINKPFESEIKLEKLNKL 1551

Search completed: August 13, 2003, 19:12:39

Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 19:08:31 ; Search time 11 seconds
(without alignments)
581.421 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MATKSMGDIKIKKLNVL.....LAKPLTKDKIIPINQMIDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178.5	26.3	1197	1 EVGS_ECOLI	P30855 escherichia
2	176.5	28.0	1197	1 EVGS_ECO57	P84402 escherichia
3	173.5	25.6	948	1 RCSC_SALTY	Q56128 salmonella
4	172.5	25.4	948	1 RCSC_SALTY	P58662 salmonella
5	171.5	25.3	949	1 RCSC_ECOLI	P14376 escherichia
6	156.5	23.1	777	1 FRZE_MYXXA	P18769 myxococcus
7	150	22.1	622	1 SKN7_YEAST	P38889 saccharomyc
8	149.5	22.1	778	1 ARCB_ECO57	P58363 escherichia
9	149.5	22.1	778	1 ARCB_ECOLI	P22763 escherichia
10	145	21.4	1220	1 SUNI_YEAST	P39928 saccharomyc
11	143.5	21.2	712	1 SKL1_YEAST	Q07084 saccharomyc
12	142	20.9	907	1 GACS_PSESY	P48027 pseudomonas
13	140.5	20.7	226	1 DCTR_BACSU	P96602 bacillus su
14	140.5	20.7	230	1 DCTR_BACHD	Q9K998 bacillus ha
15	134	19.8	119	1 CHEY_BACSU	P24072 bacillus su
16	134	19.8	1238	1 BVGS_BORPE	P16575 bordetella
17	133.5	19.7	228	1 DCTR_BACME	P39486 bacillus me
18	133.5	19.7	918	1 BARA_ECOLI	P26607 escherichia
19	133.5	19.5	131	1 YSOL_PLEBO	P51586 plectonema
20	132.5	19.5	918	1 BARA_SHIFL	P59342 shigella fl
21	132	19.5	859	1 LUXQ_VIBHA	P54302 vibrio harv
22	131.5	19.4	441	1 ZRAR_SALTY	Q82333 salmonella
23	131.5	19.4	441	1 ZRAR_SALTY	P25852 salmonella
24	130	19.2	1238	1 BVGS_BORPA	P40330 bordetella
25	128.5	19.0	849	1 LUXN_VIBHA	P34301 vibrio harv
26	127.5	18.8	522	1 MCS4_SCHPO	P87323 schizosacch
27	127	18.7	1238	1 BVGS_BORBR	P26762 bordetella
28	126.5	18.7	227	1 CPXR_HAEIN	P44895 haemophilus
29	125.5	18.5	443	1 ZRAR_LEOX	Q9apd9 klebsiella
30	124	18.3	144	1 CHEY_TREPA	P96126 treponema p
31	124	18.3	539	1 PRRI_SCHPO	O14283 schizosacch
32	122.5	18.1	441	1 ZRAR_ECOLI	P43775 escherichia
33	122	18.0	248	1 ALGR_PSEAE	P26275 pseudomonas

RESULT 1

ID	EVGS_ECOLI	STANDARD:	PRT:	1197 RA.
AC	P30855; P77644; Q9RF36; Q9RF37;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Sensor protein evgs precursor (EC 2.7.3.-)			
GN	EVGS OR B2370.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=94171083; PubMed=8125343;			
RA	Utsumi R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki S.,			
RA	Nakagawa H., Miwa A., Tanabe H., Noda M.;			
RT	"Newly identified genes involved in the signal transduction of			
RT	Escherichia coli K-12.";			
RL	Gene 140:73-77(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=93173621; PubMed=1289796;			
RA	Utsumi R., Katayama S., Ikeda M., Nakagawa H., Miwa A.,			
RA	Taniguchi M., Noda M.;			
RT	"Cloning and sequence analysis of the evgAS genes involved in signal			
RT	transduction of Escherichia coli K-12.";			
RN	[3]			
RP	Nucleic Acids Symp. Ser. 27:149-150(1992).			
RP	SEQUENCE FROM N.A. (VARIANTS EVGS1 AND EVGS4).			
RC	STRAIN=K12;			
RX	MEDLINE=2037813; PubMed=10923791;			
RA	Kato A., Ohnishi H., Yamamoto K., Furuta E., Tanabe H., Utsumi R.;			
RT	"Transcription of emrK is regulated by the EvgA-Evgs two-component			
RT	system in Escherichia coli K-12.";			
RN	[4]			
RP	Biosci. Biotechnol. Biochem. 64:1203-1209(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1234-1238(1997).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=97349980; PubMed=9205837;			
RA	Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,			
RA	Itch T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,			
RA	Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,			

Q8x613 escherichia
P10957 escherichia
O34594 bacillus su
Q45994 cauliobacter
P16244 escherichia
O44006 alcaligenes
P49246 xanthomonas
Q56312 thermocoga
P51358 porphyra pu
P43501 pseudomonas
O06065 escherichia
O78428 guillardia

ALIGNMENTS

Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T.,
 RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";
 RL DNA Res. 4:91-113(1997).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=98194702; PubMed=9535079;
 RA Petraud A.-L., Kimmel B., Weiss V., Gross R.;
 RT "Specificity of the BvgAS and EvgAS phosphorelay is mediated by the C-terminal HPT domains of the sensor proteins.";
 RL Mol. Microbiol. 27:875-887(1998).
 CC -!- FUNCTION: Member of the two-component regulatory system evgs/evgA. Phosphorylates evgA via a four-step phosphorelay in response to environmental signals.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (Probable).
 CC -!- PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp in the receiver domain and to a His in the secondary transmitter domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 HPT domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D14008; BAA03108.1; .
 DR EMBL; AF201840; AAF17563.1; .
 DR EMBL; AF201841; AAF17564.1; .
 DR EMBL; AE000325; AAC75429.1; .
 DR EMBL; D90867; BAA16241.1; .
 DR PIR; G5010; G65010.
 DR HSP; P06143; IUDR.
 DR Ecogen; EGI1610; evgs.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR004358; Bact_sens_pt-C.
 DR InterPro; IPR003661; His_kinA.
 DR InterPro; IPR005467; His_kinase.
 DR InterPro; IPR002570; Hpt.
 DR InterPro; IPR001789; Response_reg.
 DR InterPro; IPR001311; SBP_glu_receptor.
 DR InterPro; IPR001638; SBP_bac_3.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00512; HlsKA; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR Pfam; PF00497; SBP_bac_3; 1.
 DR PRINTS; P00344; BCTELSENSOR.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HlsKA; 1.
 DR SMART; SM00073; HPT; 1.
 DR SMART; SM00062; PBPB; 2.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50109; HIS_KIN; 1.
 DR PROSITE; PS50894; HPT; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Transferase; Kinase; Phosphorylation;
 KW Transmembrane; Inner membrane; Signal; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 1197
 FT DOMAIN 22 325
 FT TRANSMEM 326 346
 FT DOMAIN 347 557
 FT TRANSMEM 538 558
 FT TRANSMEM 558

FT DOMAIN 559 1197
 FT DOMAIN 718 938
 FT DOMAIN 960 1074
 FT DOMAIN 1098 1197
 FT MOD_RES 721 721
 FT MOD_RES 1009 1009
 FT MOD_RES 1137 1137
 FT VARIANT 577 577
 FT VARIANT 701 701
 FT CONFLICT 152 152
 FT CONFLICT 242 243
 FT CONFLICT 275 275
 FT CONFLICT 420 421
 FT CONFLICT 739 739
 FT CONFLICT 758 758
 FT CONFLICT 761 761
 FT CONFLICT 877 877
 FT CONFLICT 1045 1045
 FT CONFLICT 1074 1074
 FT CONFLICT 1197 AA; E8E1DE0F797B1278 CRC64;
 SQ SEQUENCE 1197 AA; 134742 MW; E8E1DE0F797B1278 CRC64;
 Query Match 26.3%; Score 178.5; DB 1; Length 1197;
 Best Local Similarity 34.4%; Pred. No. 2.9e-07;
 Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;
 Qy 12 IKKLNVLIVDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71
 Db 955 LPEKLSIIIDDDPTNLLKRLNLLGVDVDEATDGVQA--LHKVSMQHYDILLITDVM 1012
 Qy 72 PERDGVSTFKLEMEVKSNIQVTSIADNEERRAFMEAGLHCLAKPLTKDKIIPILN 131
 Db 1013 PNMDGFELTKRLQNSNPIMGLTANA-QANEREKGLSCGMNLCDFRLILDVLKTHLS 1071
 Qy 132 QL 133
 Db 1072 QL 1073
 RESULT 2
 EVGS_ECO57 STANDARD; PRT; 1197 AA.
 ID EVGS_ECO57 STANDARD; PRT; 1197 AA.
 AC P58402;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sensor protein evgs precursor (EC 2.7.3.-).
 GN EVGS OR Z3632 OR ECS3249.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=2115231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
 RT

CYTOPLASMIC (POTENTIAL).
 HISTIDINE KINASE.
 RESPONSE REGULATORY.
 HPT.
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 PHOSPHORYLATION (BY SIMILARITY).
 PHOSPHORYLATION (BY SIMILARITY).
 E -> S (IN EVGS1; CONSTITUTIVELY ACTIVE).
 L -> F (IN REF. 1 AND 2).
 FF -> PL (IN REF. 1 AND 2).
 W -> R (IN REF. 1 AND 2).
 SQ -> FE (IN REF. 1 AND 2).
 G -> D (IN REF. 1 AND 2).
 G -> K (IN REF. 1 AND 2).
 L -> V (IN REF. 1 AND 2).
 S -> L (IN REF. 1 AND 2).
 R -> H (IN REF. 1 AND 2).
 H -> Y (IN REF. 1 AND 2).


```

RESULT 5
RCSC_ECOLI
ID RCSC_ECOLI STANDARD: PRT: 949 AA.
AC F14376; P76457; P97170; P97202; Q47586;
DT 01-JAN-1990 (Rel. 13, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
DE component C).
GN RCSC OR B2218.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12.
RX MEDLINE=90130299; PubMed=2404948;
RA Stout V., Gottesman S.;
RT "RcsB and RcsC: a two-component regulator of capsule synthesis in
RT Escherichia coli.";
RL J. Bacteriol. 172:659-669(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O9:K30:H12;
RX MEDLINE=93374832; PubMed=8366025;
RA Jayaratne P., Keenleyside W.J., MacLachlan P.R., Dodgson C.,
RA Whitfield C.;
RT "Characterization of rcsB and rcsC from Escherichia coli O9:K30:H12
RT and examination of the role of the rcs regulatory system in
RT expression of group I capsular polysaccharides.";
RL J. Bacteriol. 175:5384-5394(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 450-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -1- FUNCTION: Member of the two-component regulatory system rcsC/rcsB
CC involved in the regulation of the expression of genes involved in
CC colanic acid capsule synthesis. RcsC probably functions as a
CC membrane-associated protein kinase that phosphorylates rcsB in
CC response to environmental signals.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- PTM: Activation probably requires a transfer of a phosphate group
CC between a His in the transmitter domain and an Asp of the receiver
CC domain (By similarity).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
CC -1- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -1- SIMILARITY: Contains 1 response regulatory domain.
CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 808.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M28242; AAA24503.1; ALT_INIT.
CC EMBL; L11272; AAA24505.1; ALT_INIT.
CC EMBL; AE000311; AAC75278.1; ALT_INIT.
CC EMBL; D90850; BAA16001.1; ALT_FRAME.
CC EMBL; D90850; BAA16006.1; ALT_FRAME.
CC EMBL; D90851; BAA16009.1; ALT_FRAME.
CC EMBL; D90851; BAA16014.1; ALT_FRAME.
CC HSSP; P06143; IUDR.
CC EcoGene; EG10822; rcsC.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR004358; Bact_sens_pr_C.
CC InterPro; IPR003661; His_kinA.
CC InterPro; IPR005467; His_kinase.
CC InterPro; IPR000014; PAS_domain.
CC InterPro; IPR001789; Response_reg.
CC Pfam; PF02518; HATPase_C; 1.
CC Pfam; PF00512; HiskA; 1.
CC Pfam; PF00072; response_reg; 1.
CC PRINTS; PR00344; BCTRLSENSOR.
CC ProDom; PD000039; Response_reg; 1.
CC SMART; SM00387; HATPase_C; 1.
CC SMART; SM00388; HiskA; 1.
CC SMART; SM00091; PAS; 1.
CC SMART; SM00448; REC; 1.
CC PROSITE; PS0109; HIS_KIN; 1.
CC PROSITE; PS0112; PAS; FALSE_NEG.
CC PROSITE; PS0110; RESPONSE_REGULATORY; 1.
CC Sensory transduction; Transfrase; Kinase; Bacterial capsule;
CC Inner membrane; Transmembrane; Phosphorylation; Complete proteome.
CC KW CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 19
FT TRANSMEM 20 41
FT DOMAIN 42 313
FT TRANSMEM 314 335
FT DOMAIN 336 949
FT TRANSMEM 337 425
FT DOMAIN 476 692
FT DOMAIN 826 940
FT MOD_RES 479 479
FT MOD_RES 875 875
FT VARIANT 315 315
FT VARIANT 776 776
FT VARIANT 890 890
FT VARIANT 938 938
FT VARIANT 948 948
FT CONFLICT 129 130
FT CONFLICT 935 935
SQ SEQUENCE 949 AA; 106506 MW; E37E9D70EC944A78 CRC64;
Query Match 25.3%; Score 171.5; DB 1; Length 949;
Best Local Similarity 33.9%; Pred. No. 8.6e-07;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;
QY 18 VLIVDDDLPLNLIHEKIIKAGISQIANGGEAVIHRDGGSGFDLILMDKEMPERDGV 77
Db 827 ILVDDHPINRRLADQLGSLGYCKTANGDGVDAIENVL--SKNHIDIVLSDVNNPNMDGY 884
QY 78 SITKLRNEVYSKMGVTSIADNEERAFNEAGLNHCLAKPLTKDKI 126
Db 885 RLTORQLRGLPLPVIQVGTANALAEKQRC-LESGMDSCLSKPKVTLDOI 932
RESULT 6
FRZE_MYXXA
ID FRZE_MYXXA STANDARD: PRT: 777 AA.
AC P18769;
DT 01-NOV-1990 (Rel. 16, Created)

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01-NOV-1990 (Rel. 16, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Gliding motility regulatory protein (EC 2.7.3.-).
 FRZE.

GN Myxococcus xanthus.
 OS Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 OC Cytochromatetaceae; Myxococcaceae; Myxococcus.
 OX NCBI_TaxID=34;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90332690; PubMed=2165608;
 RA McCleary W.R., Zusman D.R.;
 RT "FrzE of Myxococcus xanthus is homologous to both CheA and CheY of
 RL Salmonella typhimurium";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5898-5902(1990).
 [2]
 RN PHOSPHORYLATION OF HIS-49.
 RX MEDLINE=91072208; PubMed=2123853;
 RA McCleary W.R., Zusman D.R.;
 RT "Purification and characterization of the Myxococcus xanthus FrzE
 RL protein shows that it has autophosphorylation activity";
 RL J. Bacteriol. 172:6661-6668(1990).
 CC -!- FUNCTION: FRZE IS INVOLVED IN A SENSORY TRANSDUCTION PATHWAY THAT
 CC CONTROLS THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING THAT
 CC DIRECTION. FRZE SEEMS TO BE CAPABLE OF AUTOPHOSPHORYLATING ITSELF
 CC ON AN HISTIDINE RESIDUE AND THEN TO TRANSFER THAT GROUP TO AN
 CC ASPARTATE RESIDUE IN THE C-TERMINAL PART OF THE PROTEIN.
 CC -!- SIMILARITY: Contains 1 cheW-like domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -!- SIMILARITY: Contains 1 HPT domain.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC -----
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 CC -----
 DR EMBL; M35192; AAA25396.1; -
 DR PIR; A35966; A35966.
 DR HSP; Q56310; LB30.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR002545; Chew.
 DR InterPro: IPR005467; His_kinase.
 DR InterPro: IPR002570; Hpt.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam; PF01584; Chew; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF01627; Hpt; 1.
 DR Pfam; PF00072; response_reg; 1.
 DR PRINTS; PR00344; BCTRLSENSOR.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00260; Chew; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00073; HPT; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS00851; CHEW; 1.
 DR PROSITE; PS0109; HIS_KIN; 1.
 DR PROSITE; PS00894; HPT; 1.
 DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
 KW Sensory transduction; Transferase; Kinase; Phosphorylation.
 FT DOMAIN 1 108 HPT
 FT DOMAIN 270 509 HISTIDINE KINASE.
 FT DOMAIN 511 645 CHEW-LIKE.
 FT DOMAIN 660 776 RESPONSE REGULATORY.
 FT MOD_RES 49 49 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT DOMAIN 130 197 ALA/PRO-RICH (POSSIBLE HINGE REGION).
 CC SEQUENCE 777 AA; 83189 MW; 9912BD40991C69E5 CRC64;

Query Match

23.1%; Score 156.5; DB 1; Length 777;

Best Local Similarity 35.2%; Pred. No. 1.2e-05;
 Matches 38; Conservative 27; Mismatches 38; Indels 5; Gaps 3;
 QY 14 KKLNVLIIVDDDDPLNLIITHEKIIKAIGISQTANGGEAVIIRHGGSSFDLILMKEMPE 73
 DB 657 KRLRVLLVDDSPITARATEGALVKALGHSVEEAQGEAVY--KVQNTYDLILTDVQMPK 714
 QY 74 RDGVSTTKKLRMEVKSMI--GVVTSIADNEFEERRAFMEAGLNHCLAK 119
 DB 715 LDGFSLARURKSTPAVARIPVILSLASPEDRRG--LDAGADAYLVK 761
 RESULT 7
 SKN7_YEAST STANDARD; PRT; 622 AA.
 AC P38889; P39747;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative transcription factor SKN7 (POS9, protein).
 GN SKN7 OR POS9 OR BRY1 OR YHR206W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94042854; PubMed=8226533;
 RA Brown J.L., North S., Bussey H.;
 RT "SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
 RT beta-glucan assembly, encodes a product with domains homologous to
 RT prokaryotic two-component regulators and to heat shock transcription
 RT factors";
 RT J. Bacteriol. 175:6908-6915(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Krens B., Charizanis C., Entian K.-D.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288c / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kueba T., Hillier L., Jier M., Johnston L., Langston V.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nhan M., Rifkin L., Riles L., St. Peter H., Trevasakis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII";
 RL Science 265:2077-2082(1994).
 [4]
 RP FUNCTION, AND MUTAGENESIS.
 RX MEDLINE=95045411; PubMed=7957083;
 RA Brown J.L., Bussey H., Stewart R.C.;
 RT "Yeast Skn7p functions in a eukaryotic two-component regulatory
 RT pathway";
 RL EMBO J. 13:5186-5194(1994).
 CC -!- FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT
 CC MAY FUNCTION IN A TWO-COMPONENT SIGNAL TRANSDUCTION PATHWAY THAT
 CC ACTS IN PARALLEL WITH THE PKC1 CASCADE TO REGULATE GROWTH AT THE
 CC CELL SURFACE.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC -----
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FT DOMAIN 153 223 PAS.
FT DOMAIN 226 278 PAC.
FT DOMAIN 289 507 HISTIDINE KINASE.
FT DOMAIN 527 643 RESPONSE REGULATORY.
FT DOMAIN 678 771 HPT.
FT MOD_RES 292 292 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 576 576 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 717 717 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 778 AA; 88010 MW; C8AE004B007F9D30 CRC64;

Query Match 22.1%; Score 149.5; DB 1; Length 778;
Best Local Similarity 25.6%; Pred. No. 4 6e-05;
Matches 31; Conservative 40; Mismatches 47; Indels 3; Gaps 2;

QY 16 LNVLYDDPLNLIIHKIKIKAIGGISQTANNGEAVIHRDGGSSFDILMDKEMPERD 75
DB 526 LNVLYVEDIELNVARSVLEKLGNSVDVAMTKAALFMKPG--EYDVLVLDIQLPDMT 583
QY 76 GVSTTKKREMEVKSMTVGVTSIADNB-EERRAFMEAGLNHCIAKPLTKDKIPLINOLM 134
DB 584 GLDSRELTKKYPRDLPPIVLTANVLKQEVNAGDDVLSKPLSVPALMTAMKKFW 643
QY 135 D 135
DB 644 D 644

RESULT 9
ARCH_ECOLI STANDARD; PRT; 778 AA.
AC P22763;
DT 01-AUG-1991 (Rel. 19, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aerobic respiration control sensor protein arCB (EC 2.7.3.-).
GN arCB OR B3210 OR SF3250.
OS Escherichia coli, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=90355832; PubMed=2201868;
RA Iuchi S., Matsuda Z., Fujiwara T., Lin E.C.C.;
RT "The arCB gene of Escherichia coli encodes a sensor-regulator protein
RL for anaerobic repression of the arc regulon."
RN [2] Mol. Microbiol. 4:715-727(1990).
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RN [3] Science 277:1232-1244(1997).
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Ou D., Dong J.,
RA Sun L., Xue Y., Zhao Y., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RN through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [4]
RP CHARACTERIZATION.

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RC SPECIES=E.coli; STRAIN=ML5;
RX MEDLINE=97431492; PubMed=9286997;
RA Georgellis D., Lynch A.S., Lin E.C.C.;
RT "In vitro phosphorylation study of the arc two-component signal
RL transduction system of Escherichia coli."
RN J. Bacteriol. 179:5429-5435(1997).
RP [5]
RC CHARACTERIZATION.
RC SPECIES=E.coli; STRAIN=ML5;
RX MEDLINE=99047671; PubMed=9830034;
RA Georgellis D., Kwon O., De Wulf P., Lin E.C.C.;
RT "Signal decay through a reverse phosphorelay in the arc two-component
RL signal transduction system."
RN J. Biol. Chem. 273:32864-32869(1998).
RN [6]
RC MUTAGENESIS OF HIS-292; ASP-576 AND HIS-717.
RC SPECIES=E.coli; STRAIN=K12 / MC4100;
RX MEDLINE=20309722; PubMed=10851007;
RA Kwon O., Georgellis D., Lin E.C.C.;
RT "Phosphorelay as the sole physiological route of signal transmission
RL by the arc two-component system of Escherichia coli."
RN J. Bacteriol. 182:3858-3862(2000).
RN [7]
RC X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS) OF 660-778.
RC SPECIES=E.coli;
RX MEDLINE=97207018; PubMed=9054511;
RA Kato M., Mizuno T., Shimizu T., Hakoshima T.;
RT "Insights into multistep phosphorelay from the crystal structure of
RL the C-terminal HPT domain of ArcB."
RN Cell 88:717-723(1997).
RN [8]
RC X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 659-776 IN COMPLEX WITH CHEY.
RC SPECIES=E.coli;
RX MEDLINE=98437504; PubMed=9761838;
RA Kato M., Mizuno T., Hakoshima T.;
RT "Crystallization of a complex between a novel C-terminal transmitter,
RL HPT domain, of the anaerobic sensor kinase ArcB and the chemotaxis
RN Acta Crystallogr. D 54:140-142(1998).
RN [9]
RC X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS) OF 659-776.
RC SPECIES=E.coli;
RX MEDLINE=2003135; PubMed=10531481;
RA Kato M., Mizuno T., Shimizu T., Hakoshima T.;
RT "Refined structure of the histidine-containing-phosphotransfer (HPT)
RL domain of the anaerobic sensor kinase ArcB from Escherichia coli at
RN 1.57-A resolution."
RX Acta Crystallogr. D 55:1842-1849(1999).
CC -!- FUNCTION: Member of the two-component regulatory system arcB/arcA.
CC Sensor-regulator protein for anaerobic repression of the arc
CC modulon. Activates arcA via a four-step phosphorelay. ArcB can
CC also dephosphorylate arcA by a reverse phosphorelay involving His-
CC 717 and Asp-576.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- PTM: Activation requires a sequential transfer of a phosphate
CC group from a His in the primary transmitter domain, to an Asp in
CC the receiver domain and to a His in the secondary transmitter
CC domain.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC -!- SIMILARITY: Contains 1 HPT domain.
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -!- SIMILARITY: Contains 1 response regulatory domain.
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DR EMBL; X53315; CAA37397.1; -
DR EMBL; U18997; AAR58012.1; -
DR EMBL; AE000400; AAC76242.1; -
DR EMBL; AE015336; AAN47115.1; -
DR PIR; D65112; RGEAR.
DR PDB; 1A0B; 18-MAR-98.
DR PDB; 2A0B; 17-JUN-98.
DR PDB; 1BDJ; 11-MAY-99.
DR PDB; 1FR0; 31-DEC-02.
DR EcoGen; EGI0062; atcb.
DR InterPro; IPR003594; Atbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR000700; PAS-assoC.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HsKA; 1.
DR Pfam; PF00989; PAS; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PD00344; BCTLSNSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00389; HsKA; 1.
DR SMART; SM00073; HPT; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00446; REC; 1.
DR TIGRFS; TIGR00229; sensory_box; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0894; HPT; 1.
DR PROSITE; PS0113; PAC; 1.
DR PROSITE; PS0112; PAS; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Sensory transduction; Transferrase; Kinase; Phosphorylation;
DR Transmembrane; Inner membrane; Transcription regulation; 3D-structure;
DR Complete proteome.
FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 26 46 POTENTIAL.
FT DOMAIN 47 57 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 POTENTIAL.
FT DOMAIN 79 778 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 223 PAS.
FT DOMAIN 226 278 PAC.
FT DOMAIN 289 507 HISTIDINE KINASE.
FT DOMAIN 527 643 RESPONSE REGULATORY.
FT DOMAIN 678 771 HPT.
FT MOD_RES 292 292 PHOSPHORYLATION (AUTO-).
FT MOD_RES 576 576 PHOSPHORYLATION (PROBABLE).
FT MUTAGEN 292 292 H->Q: LOSS OF ACTIVITY.
FT MUTAGEN 576 576 D->A: LOSS OF ACTIVITY.
FT MUTAGEN 717 717 H->Q: LOSS OF ACTIVITY.
FT CONFLICT 469 470 MISSING (IN REF. 2).
SQ SEQUENCE 778 AA; 87982 MW; DD61EA6ECF95AD30 CRC64;
Query Match 22.1%; Score 149.5; DB 1; Length 778;
Best Local Similarity 25.6%; Pred. No. 4.6e-05;
Matches 31; Conservative 40; Mismatches 47; Indels 3; Gaps 2;
QY 16 LNVLLVDDPLNLITHEKIKAIGGISOTANNGEAVIIHRDGGSPDLIMDKEMPERD 75
DB 526 LNVLLVEDIELNVTVARSVLEKLSGVDMVTGKKALEMFPG--EYDLVLDIQLPDMT 583
QY 76 GVSTTKKREMEYKMGVGTSLADNE--EERRAFMEAGLNHCLAKPLTKDKIIPLINOLM 134
DB 584 GLDISRELTKRYPRDPLPLVALTNVLRKDKQEYLNAGMDVLSPLSVPAITAMIKKF 643
QY 135 D 135
DB 644 D 644

RESULT 10
SLN1_YEAST
ID SLN1_YEAST STANDARD; PRT; 1220 AA.
AC P39328;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Osmolarity two-component system protein SLN1 (EC 2.7.3.-).
GN SLN1 OR YPD2 OR YIL147C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / YPH1;
RX MEDLINE=94024010; PubMed=8211183;
RA Ota I.M., Varshavsky A.;
RT "A yeast protein similar to bacterial two-component regulators.";
RL Science 262:566-569(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX PubMed=9169870;
RA Churche C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA Moulton S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrett B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL Nature 387:84-87(1997).
RN [3]
RP MUTAGENESIS OF HIS-576 AND ASP-1144.
RX MEDLINE=94239498; PubMed=8183345;
RA Maeda T., Margler-Murphy S.M., Saito H.;
RT "A two-component system that regulates an osmosensing MAP kinase
cascade in yeast.";
RL Nature 369:242-245(1994).
CC -1- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
CC SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
CC EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK22->
CC PBS2->HOG1 PATHWAY. INACTIVE SLN1 ALLOWS THE UNPHOSPHORYLATED SSK1
CC PROTEIN TO ACTIVATE SSK2 AND SSK22, TWO MAPKKS THAT FURTHER
CC STIMULATE THE PBS2-HOG1 MAPK CASCADE. IN LOW OSMOLARITY MEDIA,
CC THE ACTIVED SLN1 HISTIDINE KINASE REPRESSSES THE ACTIVATION OF THE
CC PBS2-HOG1 KINASE CASCADE THROUGH PHOSPHORYLATION OF SSK1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
CC BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND AN ASP OF THE RECEIVER
CC DOMAIN.
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
CC -1- SIMILARITY: Contains 1 response regulatory domain.
CC -----
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CC -----
DR EMBL; Z38059; CAA86131.1; -
DR EMBL; U01835; AAC48912.1; -
DR PIR; S48387; S48387.
DR HSP; P06143; IUDR.
DR SSD; S0001409; SLN1.
DR GO; GO:0007234; P:osmosensory signaling pathway via two-compo. . . ; IDA.
DR GO; GO:0042542; P:response to hydrogen peroxide; IMP.
DR InterPro; IPR003594; Atbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.

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DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00512; HSKA; 1.
DR Pfam: PF00072; response_reg; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR PRODOM: PD000039; Response_reg; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HSKA; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE: PS01109; HIS_KIN; 1.
DR PROSITE: PS01110; RESPONSE_REGULATORY; 1.
DR Sensory transduction; Transferase; Kinase; Phosphorylation;
KW Transmembrane.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 POTENTIAL.
FT DOMAIN 47 333 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 334 354 POTENTIAL.
FT DOMAIN 355 1220 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 573 928 HISTIDINE KINASE.
FT DOMAIN 1089 1210 RESPONSE REGULATOR.
FT MOD_RES 576 576 PHOSPHORYLATION (AUTO-) (PROBABLE).
FT MOD_RES 1144 1144 PHOSPHORYLATION (PROBABLE).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 576 576 H->O: INACTIVE.
FT MUTAGEN 891 891 G->D: SLOW GROWTH, SLN1-1 MUTANT.
FT MUTAGEN 1144 1144 D->N: INACTIVE.
SQ SEQUENCE 1220 AA; 134434 MW; 45FFE24A8165486B CRC64;

Query Match 21.4%; Score 145; DB 1; Length 1220;
Best Local Similarity 29.0%; Pred. No. 0.00019;
Matches 40; Conservative 40; Mismatches 44; Indels 14; Gaps 6;

QY 8 DIEKTKKLNVLIVDDPLNLIIEKIIKA---IGGIS--QTANNSEEA---VRIHDDG 59
DB 1080 DDKNKETSVKILVEDNHVN---QEVTKRLNLEGIENTELACDGOEADFKVELTSKG 1135
QY 60 SFFDILDKEMPERDGVSTTKKL-REMEVKSMIVGVTSIADNEERFAPAEAGLNHCLA 118
DB 1136 ENYNIEMFDMQPKYDGLLSTKMIRDLGYTSPIVALTAADSDNIKEC-LESSMNGELS 1194
QY 119 KPLTKDKLIPLINQMDA 136
DB 1195 KPIKRPKLTILTEPCAA 1212

RESULT 11
SSK1_YEAST STANDARD; PRT; 712 AA.
AC Q07084; Q07909;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Osmolarity two-component system protein SSK1.
GN SSK1 OR YLR006C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RX MEDLINE=94239498; PubMed=8183345;
RA Maeda T., Wurgler-Murphy S.M., Saito H.;
RT "A two-component system that regulates an osmosensing MAP kinase
RL cascade in yeast.";
RL Nature 369:242-245(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313267; PubMed=9169871;

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RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansonge W.,
RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharte M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
CC -!- SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
CC EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK22->
CC PBS2->HOG1 PATHWAY. THE UNPHOSPHORYLATED FORM OF SSK1 ACTIVATES
CC SSK2 AND SSK22, TWO MAPKKS THAT FURTHER STIMULATE THE PBS2-HOG1
CC MAPK CASCADE. IN LOW-OSMOLARITY MEDIA, IS INHIBITED THROUGH THE
CC PHOSPHORYLATION BY SLN1.
CC -!- SUBUNIT: SEEMS TO INTERACT WITH SSK2 AND SSK22.
CC -!- SUBCELLULAR LOCATION: cytoplasmic (potential).
CC -!- SIMILARITY: Contains 1 response regulatory domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L26523; AAA35100.1; -.
CC EMBL; Z73178; CAA97528.1; -.
DR PIR; S64828; S64828.
DR SGD; S000396; SSK1.
DR GO; GO:0007234; P:osmosensory signaling pathway via two-compo. . . ; IDA.
DR GO; GO:0042542; P:response to hydrogen peroxide; IMP.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg; 1.
DR PRODOM; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01110; RESPONSE_REGULATORY; 1.
KW Sensory transduction; Phosphorylation.
FT DOMAIN 505 647 RESPONSE REGULATORY.
FT MOD_RES 554 554 PHOSPHORYLATION (PROBABLE).
FT MUTAGEN 554 554 D->N: ACTIVATES.
FT CONFLICT 181 181 P -> S (IN REF. 1).
SQ SEQUENCE 712 AA; 78529 MW; 33B2DBB4FCF2528A CRC64;

Query Match 21.2%; Score 143.5; DB 1; Length 712;
Best Local Similarity 27.9%; Pred. No. 0.00013;
Matches 39; Conservative 26; Mismatches 42; Indels 31; Gaps 3;

QY 10 EKIKKKLNVLIVDDPLNLIIEKIIKAIGISQTANNSEEAIVIIHDDGSGSFDLIMDK 69
DB 498 EKVPKPNVLIVDINVAINGALISGLRKHKISYKLAKNGQEAIVNKGEG--LHLIFMDL 555
QY 70 EMPERDGVSTTKKLREMEVKS-----MIVGVTSIADN 101
DB 556 QLPVLISGIEAAKQIRDFEKQNGIGIQKSLANSHNLEKGTGSKRFSQAPVLIIVALTASNQ 615
QY 102 EEERRAFMEAGLNHCLAKPL 121
DB 616 MDRKALL-SGCNDYLTKPV 634

RESULT 12
GACS_PSESY
ID GACS_PSESY STANDARD; PRT; 907 AA.
AC P48027;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

```

28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein gacs (EC 2.7.3.-).
GACS OR LEMA.
Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=321;
[1]
SEQUENCE FROM N.A.
MEDLINE=92234961; PubMed=1314807;
Hrabak E.M., Willis D.K.;
"The lema gene required for pathogenicity of Pseudomonas syringae pv.
syringae on bean is a member of a family of two-component
regulators."; 174:3011-3020(1992).
CC -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
GACS/GACS(LEMA). MAY BE INVOLVED IN LESION FORMATION, SWARMING AND
IN THE PRODUCTION OF EXTRACELLULAR PROTEASE, SYRINGOMYCIN AND N-
ACYL-L-HOMOSERINE LACTONE (ACYL-HSL). REQUIRED FOR PATHOGENICITY
ON BEAN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(Probable).
CC -!- PTM: Activation requires a sequential transfer of a phosphate
group from a His in the primary transmitter domain, to an Asp in
the receiver domain and to a His in the secondary transmitter
domain (By similarity).
CC -!- SIMILARITY: Contains 1 HAMP domain.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
CC -!- SIMILARITY: Contains 1 HPT domain.
CC -!- SIMILARITY: Contains 1 response regulatory domain.
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or send an email to license@isb-sib.ch).
CC EMBL: M80477; AAA25877.1; -
DR HSP; P06143; LUDR.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003660; HAMP.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR002570; Hpt.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF00672; HAMP; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00512; HSKA; 1.
DR Pfam: PF01627; Hpt; 1.
DR Pfam: PF00072; response_reg; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00304; HAMP; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HSKA; 1.
DR SMART: SM00073; HPT; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE: PS00885; HAMP; 1.
DR PROSITE: PS0109; HIS_KIN; 1.
DR PROSITE: PS00894; HPT; 1.
DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
KW Sensory transduction; Transferase; Kinase; Phosphorylation;
Transmembrane; Inner membrane.
FT TRANSMEM 9 25 POTENTIAL.
FT TRANSMEM 84 101 POTENTIAL.
FT TRANSMEM 159 178 POTENTIAL.
FT DOMAIN 182 234 HAMP.
FT DOMAIN 281 502 HISTIDINE KINASE.
FT DOMAIN 658 777 RESPONSE REGULATORY.
FT DOMAIN 814 907 HPT.

FT MOD_RES 284 284 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 707 707 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 853 853 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 907 AA; 99195 MW; 5B9F4663DAF3492C CRC64;
Query Match 20.9%; Score 142; DB 1; Length 907;
Best Local Similarity 27.6%; Pred. No. 0.00023;
Matches 35; Conservative 33; Mismatches 33; Indels 26; Gaps 4;
QY 18 VLVIVDDPLNLIHKEIKIAGGISTQANNGEEAVIHRDGG-----SFFDIILMD 68
Db 659 VLVYDDNFANLLVQTLLLEDMG-----AEVAVEGGYAANVAVQCEAFDLVMD 707
QY 69 KEMPERDGVSTKKLREMEVKS-----MIQVTSIADNEEERAFMEAGLNHCLAPLTK 123
Db 708 VQPMGMDGRQATEIRAEWAEARNQSSIPVALTAHA--MANEKRSLQSGMDLYLTPRISE 766
QY 124 DKIIPLI 130
Db 767 ROLAQVV 773
RESULT 13
DCTR_BACSU
ID DCTR_BACSU STANDARD; PRT; 226 AA.
AC P96602; P94503;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable C4-dicarboxylate response regulator dctr.
GN DCTR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Lee S., Sadale Y., Ogasawara N.;
RT "A 148 kbp sequence of the region between 35 and 47 degree of the
Bacillus subtilis genome."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Koenigsstein G., Krogh S., Kumano M.,
Kobayashi Y., Koetter P., Konings S., Lauber J., Lazarevic V.,
Kurita K., Lapidus A., Lindholm S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Prescan E., Pujic P., Farnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Banchin A.;

"The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*,"
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 14-101 FROM N.A.
RC STRAIN=SB202;
RA MEDLINE=973111990; PubMed=9168601;
RX Morel-Deville F., Ehrlich S.D., Morel P.;
RT "Identification by PCR of genes encoding multiple response
regulators,"
RL Microbiology 143:1513-1520(1997).
RN [4]
RP FUNCTION, AND GENE NAME.
RC STRAIN=168;
RX MEDLINE=20170658; PubMed=10708364;
RA Asai K., Baik S.-H., Kasahara Y., Moriya S., Ogasawara N.;
RT "Regulation of the transport system for C4-dicarboxylic acids in
Bacillus subtilis,"
RL Microbiology 146:263-271(2000).
RN [5]
RP FUNCTION, MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
CC -!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
CC ESSENTIAL FOR EXPRESSION OF DCTP.
CC -!- PTM: PHOSPHORYLATED BY DCTS (PROBABLE).
CC -!- SIMILARITY: Contains 1 response regulatory domain.
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CC
CC EMBL: AB001488; BAA19283.1; -
DR EMBL: 299106; CAB12253.1; -
DR EMBL: 082580; ABA11751.1; -
DR PIR: B69771; B69771.
DR HSSP: Q56312; ITWY.
DR Subtilist; BG12074; dctr.
DR InterPro; IPR001789; Response_reg.
DR Pfam: PF00072; response_reg; 1.
DR PIRSF: PIRSF006171; RR.Citrat.malat; 1.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Sensory transduction; Transcription regulation; DNA-binding;
KW Activator; Phosphorylation; Complete proteome.
FT DOMAIN 7 123 RESPONSE_REGULATORY.
FT MOD_RES 58 58 PHOSPHORYLATION (BY SIMILARITY).
FT DNA_BIND 176 206 H-T-H MOTIF (POTENTIAL).
FT CONFLICT 24 24 F -> I (IN REF. 3).
SQ SEQUENCE 226 AA; 25539 MW; 018115B14E9EF47D CRC64;

Query Match 20.7%; Score 140.5; DB 1; Length 226;
Best Local Similarity 25.9%; Pred. No. 6.7e-05;
Matches 30; Conservative 39; Mismatches 42; Indels 5; Gaps 3;

QY 13 KKLNVIVDDPLNLIIHEKIIKAIGIS--QTANNGEAAVTHRDGGSFDFLLMDXE 70
DB 3 RKEWVLLIEDPMVQVNRMFVEKLSGFTIVGTATGEBGVKTR--LQPDLLIDIFMPK 60

QY 71 MPERGVSTTKKREMEVKSMIVGVTSLADNEERRAFMEAGLNHCLAKPLTKDKI 126
DB 61 MPKDGKIKTLQIRKQKLEVDVI-VVSAAKDKETISLMQNGAVDVIYLPKPKLERM 115

RESULT 14
DCTR_BACHD
ID DCTR_BACHD STANDARD; PRT; 230 AA.
AC Q9K998;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Probable C4-dicarboxylate response regulator dctr.
DCTR OR BH2751.
OS *Bacillus halodurans*.
GN Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A. 9153;
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*,"
RL Nucleic Acids Res. 28:4317-4331(2000).
RN [2]
RP FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
CC -!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
CC ESSENTIAL FOR EXPRESSION OF DCTP (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- PTM: PHOSPHORYLATED BY DCTS (By similarity).
CC -!- SIMILARITY: Contains 1 response regulatory domain.
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CC
CC EMBL: AP001516; BAB06470.1; -
DR PIR: G83993; G83993.
DR HSSP: PI0957; IRNL.
DR InterPro; IPR001789; Response_reg.
DR Pfam: PF00072; response_reg; 1.
DR PIRSF: PIRSF006171; RR.Citrat.malat; 1.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Sensory transduction; Transcription regulation; DNA-binding;
KW Activator; Phosphorylation; Complete proteome.
FT DOMAIN 8 124 RESPONSE_REGULATORY.
FT MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
FT DNA_BIND 183 209 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 230 AA; 26376 MW; 06FD65F46FC57D40 CRC64;

Query Match 20.7%; Score 140.5; DB 1; Length 230;
Best Local Similarity 29.4%; Pred. No. 6.9e-05;
Matches 35; Conservative 32; Mismatches 47; Indels 5; Gaps 3;

QY 16 LNVIVDDPLNLIIHEKIIKAIGG--ISQTANNGEAAVTHRDGGSFDFLLMDKEMPE 73
DB 7 IRVLLIEDPMVQVNRMFVEKLSGFTIVGTATGEBGVKTR--LQPDLLIDIFMPK 64

QY 74 RGVSTTKKREMEVKSMIVGVTSLADNEERRAFMEAGLNHCLAKPLTKDKIPLNQ 132
DB 65 QDGLSFIKQIREQYIDVDIIAATA-ANDTKITKLLRYGVMDYLVKPTFERKALATQ 122

RESULT 15
CHEY_BACSU
ID CHEY_BACSU STANDARD; PRT; 119 AA.
AC P24072; P37583;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotaxis protein chey homolog.
GN CHEY OR CHEB.
OS *Bacillus subtilis*.
GN Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / O11085;

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OM protein - protein search, using sw model

Run on: August 13, 2003, 19:09:22 ; Search time 37 seconds
(without alignments)

948,518 Million cell updates/sec

Title: US-09-646-679-15

Perfect score: 678

Sequence: 1 MATKSMGDIKIKKLNVL.....LAKPLKDKIIPLINOLMDA 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	136	10	O82445
2	538	79.4	142	10	Q9M844
3	181	26.7	1969	5	O15763
4	179.5	26.5	820	16	Q8Z63
5	178.5	26.3	1197	16	O8CVU5
6	174	25.7	394	16	Q9A3P0
7	173.5	25.6	949	16	Q8FFP9
8	173	25.5	417	2	Q9RLC7
9	171.5	25.3	933	16	Q8XE39
10	171.5	25.3	957	16	O8ZGR4
11	171	25.2	927	2	Q9ANY0
12	170	25.1	769	16	O8PQ37
13	167.5	24.7	1364	16	Q8PJN8
14	166.5	24.6	507	2	O8S663
15	163.5	24.1	1364	16	Q8P883
16	162.5	24.0	642	16	Q9A3L2

17	162.5	24.0	719	3	Q9P896
18	162.5	24.0	778	16	Q8ZB69
19	162	23.9	767	16	Q8PD62
20	161.5	23.8	148	5	Q9GTU0
21	161.5	23.8	1709	5	Q95P85
22	161	23.7	716	16	Q8O516
23	160.5	23.7	574	16	Q8D9H9
24	159.5	23.5	571	16	Q8DAE1
25	159	23.5	117	17	O28381
26	159	23.5	736	16	Q9KR16
27	159	23.5	1645	16	Q8YVW3
28	158.5	23.4	1265	3	O8NIV2
29	157	23.2	900	16	Q9AC40
30	156.5	23.1	469	2	O8NRK0
31	156	23.0	1000	17	O8TPA1
32	155	22.9	690	16	Q9A501
33	155	22.9	767	12	O8QXV7
34	154.5	22.8	122	17	O28887
35	154.5	22.8	572	16	Q9KS16
36	154	22.7	708	3	O9CLO7
37	154	22.7	848	2	Q9AEW3
38	153.5	22.6	713	16	Q9A472
39	153.5	22.6	939	2	O8KWS5
40	153	22.6	1268	2	O8QV00
41	152.5	22.5	120	17	Q48299
42	152.5	22.5	514	16	Q9ABT2
43	152.5	22.5	929	16	O8EQ02
44	152.5	22.5	935	2	Q8RME4
45	152.5	22.5	1068	16	Q8PMZ3

ALIGNMENTS

RESULT 1

O82445 PRELIMINARY: PRT: 136 AA.

AC O82445;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Response regulator protein.
OS Brassica napus (rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]

RP SEQUENCE FROM N.A.
RA Whitelaw C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;
RT "A mRNA encoding a response regulator protein from Brassica napus is
up-regulated during pod development.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
EMBL: AF057027; AAC62225.1;
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Phosphorylation; Sensory transduction.
KW SEQUENCE 136 AA; 15055 MW; DA99B768FAB3CFF5 CRC64;

Query Match 100.0%; Score 678; DB 10; Length 136;

Best Local Similarity 100.0%; Pred. No. 4.7e-52;

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATKSMGDIKIKKLNVLIVDDPLNLIIEHKIIKAIGGISQTANNGEAAVTHRDGGS 60
|||||

Db 1 MATKSMGDIKIKKLNVLIVDDPLNLIIEHKIIKAIGGISQTANNGEAAVTHRDGGS 60
|||||

QY 61 SFDLILMDKEMPERGVSTTKKLREWEVKSMIVGVTSIADNEERRAFMEAGLNHCLAKP 120
|||||

Db 61 SFDLILMDKEMPERGVSTTKKLREWEVKSMIVGVTSIADNEERRAFMEAGLNHCLAKP 120
|||||

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QY 121 LTKDKIIPILNQLMDA 136
GN |||||
Db 121 LTKDKIIPILNQLMDA 136

RESULT 2
Q9M8Y4
ID Q9M8Y4 PRELIMINARY; PRT; 142 AA.
AC Q9M8Y4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative response regulator protein (receiver component).
GN TSK12.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC TSK12 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC016829; AAF26786.1;
DR EMBL: AY085638; AAM62859.1;
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF00072; Response_reg.1.
DR ProDom: PD00039; Response_reg.1.
DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
DR Phosphorylation; Sensory transduction.
KW Phosphorylation; Sensory transduction.
SQ SEQUENCE 142 AA; 15792 MW; 57487135FF2D5238 CRC64;

Query Match 79.4%; Score 538; DB 10; Length 142;
Best Local Similarity 78.9%; Pred. No. 9.8e-40;
Matches 112; Conservative 8; Mismatches 16; Indels 6; Gaps 2;

QY 1 MATKSGDIEK-----IKKKL-NVLIVDDPLNLIIEKKIAGGISQTANNGEAEVII 54
GN |||||
Db 1 MATKSGTEKTSIEVKKKLNVLIVDDPLNRLHEMIKTIIGISQTANNGEAEVII 60

QY 55 HRDGGSSFDLIIMDKEMPERGVSTTKKLREMEVKSMIVGVTSLADNEERRAFMEAGLN 114
GN |||||
Db 61 HRDGEASFDLIIMDKEMPERGVSTTKKLREMKVTSIMVGVTSLADNEERRAFMEAGLN 120

QY 115 HCLAKPLTKDKIIPILNQLMDA 136
GN |||||
Db 121 HCLAKPLTKAKIFPLISHLFLDA 142

RESULT 3
O15763
ID O15763 PRELIMINARY; PRT; 1969 AA.
AC O15763;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hybrid histidine kinase DHKB.
GN DHKB.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KAX3;
RX MEDLINE=98248997; PubMed=9576830;
RA Zinda M.J., Singleton C.K.;
RT "The hybrid histidine kinase dhKB regulates spore germination in
RT Dictyostellium discoideum.";
RL Dev. Biol. 196:171-183(1998).
DR EMBL: AF024654; AAB1889.1;
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF02518; Harpase_c; 1.
DR Pfam: PF00512; Hiska; 1.
DR Pfam: PF00072; Response_reg.1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD000039; Response_reg.1.
DR SMART: SM00387; Harpase_c; 1.
DR SMART: SM00388; Hiska; 1.
DR SMART: SM00091; PAS; 1.
DR SMART: SM00448; REC; 1.
DR TIGRFAMS: TIGR00229; sensory_box; 1.
DR PROSITE: PS01109; HIS_KIN; 1.
DR PROSITE: PS01110; RESPONSE_REGULATORY; 1.
DR Kinase Phosphorylation; Sensory transduction.
KW Kinase Phosphorylation; Sensory transduction.
SQ SEQUENCE 1969 AA; 219025 MW; 8E7A7952A31BB52B CRC64;

Query Match 26.7%; Score 181; DB 5; Length 1969;
Best Local Similarity 35.8%; Pred. No. 5.1e-07;
Matches 48; Conservative 29; Mismatches 39; Indels 18; Gaps 5;

QY 10 EKIKKKLNVLIVDDPLNLIIEKKIAGGISQTANNGEAEVIIHRDGGSSFDLIIMDK 69
GN |||||
Db 1836 EKIEK---ILLVEDFNVNKIFSKLLDKSGYIFDVAHNGVEAVCYKKG--AYDLILMDC 1990

QY 70 EMPERGVSSTTKKLREMEVKSMI-----VGVTSLADNE--ERRAFMEAGLNHCL 117
GN |||||
Db 1891 QMPMDGFEATTATRELEKSNLIESPPSKKSHVIVALTANSYKDKQKCLSGVMNDFL 1950

QY 118 AKPL-TKDKIIPILI 130
GN |||||
Db 1951 QXPIKTSILIQMI 1964

RESULT 4
Q8EZ63
ID Q8EZ63 PRELIMINARY; PRT; 820 AA.
AC Q8EZ63;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component hybrid sensor and regulator.
GN LA3996.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE011554; AAN51193.1;
KW Complete proteome.
SQ SEQUENCE 820 AA; 94325 MW; 3DBE99966794E67D CRC64;

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Query Match          26.5%; Score 179.5; DB 16; Length 820;
Best Local Similarity 31.6%; Pred. No. 2.4e-07;
Matches 43; Conservative 29; Mismatches 49; Indels 15; Gaps 5;

QY      8 DIEK-----TKKLNVLIVDDPLNLIIEKIKAIGGISQTANNGEEAVIHRDGGSSF 62
Db      679 DLEKSFQDVYAKSTRILVAEDNETCLLIERAKLKLGYDPVIVHNGRE--VIERMQLEAF 736

QY      63 DLLIMDMKPERDGVSTTKKLREMEVKS---MIVGVTSLANDEERAFMEAGLNHCLAK 119
Db      737 DIILMDIHMEVGGIEATKWRKSNQNSFFPIIALTADA-IESKKEKYISKGMNDCLTK 795

QY      120 PLTKDKIIPLINQLMD 135
Db      796 PLD---LPILKSTLD 807

RESULT 5
Q8CVU5
ID      Q8CVU5      PRELIMINARY;      PRT; 1197 AA.
AC      Q8CVU5;
DT      01-MAR-2003 (TReMBLrel. 23, Created)
DT      01-JUN-2001 (TReMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE      Sensor protein evgs precursor (EC 2.7.3.-).
GN      EVGS OR C2906.
OS      Escherichia coli O6.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=217992;
RN      [1]
RC      SEQUENCE FROM N.A.
RP      STRAIN=O6:HI / CFT073 / ATCC 700928;
RX      MEDLINE=22388234; PubMed=12471157;
RA      Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA      Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA      Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA      Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT      "Extensive mosaic structure revealed by the complete genome sequence
RT      of uropathogenic Escherichia coli.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
RD      EMBL; AE016764; AAN81356.1; -.
RK      Transference; Complete proteome.
KW      SEQUENCE 1197 AA; 134847 MW; 5088214E7F834F06 CRC64;

Query Match          26.3%; Score 178.5; DB 16; Length 1197;
Best Local Similarity 34.4%; Pred. No. 4.6e-07;
Matches 42; Conservative 25; Mismatches 52; Indels 3; Gaps 2;

QY      12 IKKLNVLIVDDPLNLIIEKIKAIGGISQTANNGEEAVIHRDGGSSFDLIMDKEM 71
Db      955 LPEKLSILIADHPTNRLLLKRLNLLGYDVDATDGVQA--LHKVSMQHYDLLITDVM 1012

QY      72 PERDGVSTTKKLREMEVKSMTVGVTSLANDEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
Db      1013 PNMDGFELTKLRQNSSLPFWGLTANA-OANERKGLNCGMNLCLFKPLTLDVLKTHLS 1071

QY      132 QL 133
Db      1072 QL 1073

RESULT 6
Q9A3P0
ID      Q9A3P0      PRELIMINARY;      PRT; 394 AA.
AC      Q9A3P0;
DT      01-JUN-2001 (TReMBLrel. 17, Created)
DT      01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT      01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE      Sensor histidine kinase/response regulator.
GN      CC3162.
OS      Caulobacter crescentus.

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RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL: AF016763; AAN81215.1; -.
KW Transferase; Complete proteome.
SQ SEQUENCE 949 AA; 106590 MW; DF8CA47F9EBE4068 CRC64;

Query Match      25.6%; Score 173.5; DB 16; Length 949;
Best Local Similarity 33.6%; Pred. No. 9.7e-07;
Matches 37; Conservative 35; Mismatches 33; Indels 5; Gaps 3;

QY 18 VLIVDDDPNLIIHEKIIKAIGGISTQANNGEEAVI-IHRDGGSSFDLILMDKEMPERDG 76
Db 827 ILVVDHPINRLLDQGLSGYQCKTANDGVDALNVLK---NHIDIVLSDVNNPNDMG 883

QY 77 VSTTKKLEMEVKSMTVGVTSIADNEERRAFNEAGLNHCLAKPLTKDKI 126
Db 884 YRLTQRIQLGLTLPVIGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 932

RESULT 8
Q9RLC7 PRELIMINARY; PRT; 417 AA.
AC Q9RLC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative histidine kinase (Fragment).
GN GACS.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JM300;
RA Graupner S., Wackernagel W.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AJ249741; CAB56474.1; -.
DR InterPro: IPR002570; Hpt.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF00072; response_reg.1.
DR ProDom: PD000039; Response_reg.1.
DR SMART: SM00073; HPT; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE: PS01110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
FT NON_TER 1
SQ SEQUENCE 417 AA; 45749 MW; D196B4FFDDA23BB2 CRC64;

Query Match      25.5%; Score 173; DB 2; Length 417;
Best Local Similarity 32.8%; Pred. No. 4e-07;
Matches 39; Conservative 35; Mismatches 37; Indels 8; Gaps 3;

QY 17 NVLIVDDDPNLIIHEKIIKAIGGISTQANNGEEAVI-IHRDGGSSFDLILMDKEMPERDG 76
Db 169 SVLVCDDNPANLMLLETLITDGGFVAVSSQQALEVQQ--QSFDMVFVDVQMPGMDG 226

QY 77 VSTTKKLEMEVKS-----MIVGVTSIADNEERRAFNEAGLNHCLAKPLTKDKIPLI 130
Db 227 ROTTEAIRWELESQPPPLPVALTAHA-LSNERSLQSLGLDYLTKPTISEROLAQVY 284

RESULT 9
Q8XE39 PRELIMINARY; PRT; 933 AA.
AC Q8XE39;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sensor for ctr capsule biosynthesis, probable histidine kinase acting on RcsB.
GN RSCC OR Z3477 OR RCS3107.
OS Escherichia coli O157:H7.

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX Enterobacteriaceae; Escherichia.
RN [1]
RP NCBI_TaxID=83334;
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22 (2001).
DR EMBL: AE005454; AAC57353.1; -.
DR EMBL: AF002560; EAB36530.1; -.
DR HSP: F08143; 1b42.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003661; His_kinase.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF0518; HATPase_c; 1.
DR Pfam: PF00512; HSKA; 1.
DR Pfam: PF00072; response_reg.1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD000039; Response_reg.1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HSKA; 1.
DR SMART: SM00091; PAS; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE: PS01109; HIS_KIN; 1.
DR PROSITE: PS01110; RESPONSE_REGULATORY; 1.
KW Kinase; Complete proteome.
SQ SEQUENCE 933 AA; 104605 MW; 5755C05F713E561D CRC64;

Query Match      25.3%; Score 171.5; DB 16; Length 933;
Best Local Similarity 33.9%; Pred. No. 1.4e-06;
Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps 2;

QY 18 VLIVDDDPNLIIHEKIIKAIGGISTQANNGEEAVI-IHRDGGSSFDLILMDKEMPERDG 77
Db 811 ILVVDHPINRLLDQGLSGYQCKTANDGVDALNVL--SKNHIDIVLSDVNNPNDMG 868

QY 78 STTKKLEMEVKSMTVGVTSIADNEERRAFNEAGLNHCLAKPLTKDKI 126
Db 869 RLTIQRIQLGLTLPVIGVTANALAEKQRC-LESGMDSCLSKPVTLDVI 916

RESULT 10
Q8ZGR4 PRELIMINARY; PRT; 957 AA.
AC Q8ZGR4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two component sensor kinase/response regulator protein RcsC acting on RcsB.
GN RSCC OR YP01217 OR Y2971.
OS Yersinia pestis.

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RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL: AB011676; AM35383.1; -
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR002570; Hpt.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF00512; HSKA; 1.
DR Pfam: PF001627; Hpt; 1.
DR Pfam: PF00072; response_reg; 1.
DR PRINTS: PR00344; BCTRSENSOR.
DR ProDom: PD000039; Response_reg; 1.
DR TIGRFAMS: TIGR00229; sensory_box; 2.
DR PROSITE: PS0109; HIS_KIN; 1.
DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
KW Complete proteome.
SQ SEQUENCE 765 AA; 83699 MW; 37995CA40A787593 CRC64;

Query Match 25.1%; Score 170; DB 16; Length 769;
Best Local Similarity 30.5%; Pred. No. 1.5e-06;
Matches 36; Conservative 38; Mismatches 36; Indels 8; Gaps 3;

OY 14 KKLNVIVDDPNLIIHEKIIKAIGISQTANNGEAVIIHRDGGSSFDLLMDKEMPE 73
DB 495 REVILIVDDPNLIIHVAQKLLAVLFEDATDGEAA--LAMESTRYDMVFMQKPV 552

OY 74 RDGVSTTKKLEMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
DB 553 LDGYATRRWRAMETESGGRPVPIVAMTANAMAGDRERC--LAAGMDYLSKPKVAREQL 609

RESULT 13
QBPN8 PRELIMINARY; PRT; 1364 AA.
AC QBPN8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component system sensor protein.
GN XAC2492.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
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RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

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RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL: AB011887; AM37343.1; -
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR006189; CHASE.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR002570; Hpt.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-assoc_C.
DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF03924; CHASE; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00512; HSKA; 1.
DR Pfam: PF01627; Hpt; 1.
DR Pfam: PF00785; PAC; 2.
DR Pfam: PF00989; PAS; 2.
DR Pfam: PF00072; response_reg; 2.
DR PRINTS: PR00344; BCTRSENSOR.
DR ProDom: PD000039; Response_reg; 2.
DR TIGRFAMS: TIGR00229; sensory_box; 2.
DR PROSITE: PS0839; CHASE; 1.
DR PROSITE: PS0109; HIS_KIN; 1.
DR PROSITE: PS0113; PAC; 2.
DR PROSITE: PS0112; PAS; 2.
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KW Complete proteome.
SQ SEQUENCE 1364 AA; 150282 MW; F7CCA3856B7E7165 CRC64;

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DB 1033 HLLIVDDSDINCEVAQRILEGAGMTVARDGEQAVSTLKRAPNLFHLVLMQVMPVVDG 1092

OY 77 VSTTKKLEMEVKS--IVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIPLINQLM 134
DB 1093 YEATRLRQIPALASUPVIALTAGAFRPOEKA--LEAGNGFIAPFNVEELVTAIRHFL 1151

RESULT 14
QBPN8 PRELIMINARY; PRT; 507 AA.
AC QBPN8;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RCSC (Fragment).
GN RCSC.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BB2000;
RX MEDLINE=95047557; PubMed=9829920;
RA Belas R., Schneider R., Welch M.;
RA "Characterization of Proteus mirabilis precocious swarming mutants;
RT Identification of rsba, encoding a regulator of swarming behavior.";

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RL J. Bacteriol. 180:6126-6139(1998).
CC -/- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
DR EMBL; AF071215; AACB2662.1; -.
DR HSSP; P06657; 2CHF.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003661; His_KinA.
DR InterPro: IPR005467; His_Kinase.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-assoc_C.
DR InterPro: IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HiskA; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF0785; PAC; 2.
DR Pfam; PF0989; PAS; 2.
DR Pfam; PF00072; response_reg; 2.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 2.
DR TIGRFAMs; TIGR00229; sensory_box; 2.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0113; PAC; 2.
DR PROSITE; PS0112; PAS; 2.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 2.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 2.
KW Kinase; Phosphorylation; Sensory transduction; Transferase.
FT NON_TER 1
SQ SEQUENCE 507 AA; 57326 MW; F5DA2EAD9C35DEF5 CRC64;

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Best Local Similarity 36.4%; Pred. No. 1.9e-06;
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DB 397 LTVLIYDDHPINLLITDQKIGNTAEDGCCDALAFMQE--NHYDIIITDVMNPN 454
QY 76 GVSTTKKLEMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLT 122
DB 455 GYLQATTVRELSSTIFLIQVTNATAEEKQRC-IDAGMNDVCVKDVS 500

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AC Q8P883;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component system sensor protein.
GN XCC2360.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
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RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DB EMBL; AE012344; ANM41638.1; -.
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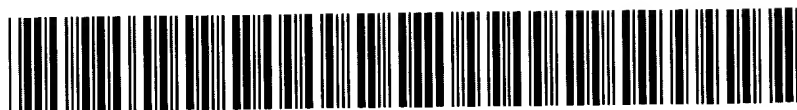
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DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR006189; CHASE.
DR InterPro: IPR003661; His_KinA.
DR InterPro: IPR005467; His_Kinase.
DR InterPro: IPR002570; Hpt.
DR InterPro: IPR001610; PAC.
DR InterPro: IPR000700; PAS-assoc_C.
DR InterPro: IPR001789; Response_reg.
DR Pfam; PF03524; CHASE; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HiskA; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF0785; PAC; 2.
DR Pfam; PF0989; PAS; 2.
DR Pfam; PF00072; response_reg; 2.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 2.
DR TIGRFAMs; TIGR00229; sensory_box; 2.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0113; PAC; 2.
DR PROSITE; PS0112; PAS; 2.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 2.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 2.
KW Complete proteome.
SQ SEQUENCE 1364 AA; 150167 MW; 48F1C5FBD9710316 CRC64;

Query Match 24.1%; Score 163.5; DB 16; Length 1364;
Best Local Similarity 30.3%; Pred. No. 1.1e-05;
Matches 36; Conservative 36; Mismatches 44; Indels 3; Gaps 3;

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DB 1034 LLLVDDSEINCEVAQRILEGAMVTVAHDGEQAVNTLKRAPDLFLHVLMDVQHPVVDGY 1093
QY 78 STTKKLEME-EVKSM-IVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQM 134
DB 1094 EATRLRQIPSLASLPVIALTAGAFRPQCEKA-LEAGMNGFIKPFNVVELVTAIRHEL 1151

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